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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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## COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

### TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the



oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example,  $^{125}\text{I}$ -labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full-length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. See, *e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a



polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody; and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177, and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may



thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic glycolide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1  $\mu$ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### EXAMPLE 1

##### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of H<sub>2</sub>O, heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l H<sub>2</sub>O. Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l H<sub>2</sub>O, mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ



ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D-1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## EXAMPLE 2

## DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42°C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTON.

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF<sup>+</sup> *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### EXAMPLE 4

##### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

#### SUMMARY

##### 1. FIELD OF THE INVENTION

The present invention relates to a method for the identification of peptides. The method involves the digestion of a sample with a proteolytic enzyme to produce peptides. The peptides are then separated by size exclusion chromatography (SEC) and analyzed by mass spectrometry (MS). The MS data is compared to a database of known peptides to identify the sample. The method is particularly useful for the identification of peptides in complex mixtures, such as those found in biological samples. The method involves the digestion of a sample with a proteolytic enzyme to produce peptides. The peptides are then separated by size exclusion chromatography (SEC) and analyzed by mass spectrometry (MS). The MS data is compared to a database of known peptides to identify the sample. The method is particularly useful for the identification of peptides in complex mixtures, such as those found in biological samples.

## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANTS: Xu, Jiangchun  
Dillon, Devin C.
  - (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE
  - (iii) NUMBER OF SEQUENCES: 224
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: SEED and BERRY LLP
    - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
    - (C) CITY: Seattle
    - (D) STATE: WA
    - (E) COUNTRY: USA
    - (F) ZIP: 98104
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE: 23-FEB-1998
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Maki, David J.
    - (B) REGISTRATION NUMBER: 31,392
    - (C) REFERENCE/DOCKET NUMBER: 210121.428C3
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (206) 622-4900
    - (B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC



ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTTGTG	CCCTTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACTGTCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGGC	TTTTGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGTCNTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNGG	AAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGA	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGAIG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCG	ATGTATTTGC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTTGACGGC	240
ACAGATGCCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTTAT	CACCACTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTAA	ACACCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCTCTG	GTGAAATTGT	TATCCGCTCA	CAATTCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTTAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCCCTT	TCCAGTCGGG	AAAACTGTCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCG	CGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCNGA			816

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGTTC	AACAGCAGAG	GTGCAGGGCG	GGGGCTCAGC	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCCTTGT	TGTGATCATG	ATGAACAACC	120

TCCTCAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTTGC	AAATACATCT	GCAAACCTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTCGCC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTCG	540
CCAGCTGGGC	GTAATANCGA	AAAGGCCCGC	ACCGATCGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNAA	ATGGGACCCC	CCTGTTACCG	CGCATTNAAC	CCCCGCNGGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCGCTCCC	TTTCNCCTTT	720
CTTCCCTTCC	TTTCNCNCCN	CTTTCCCCCG	GGGTTTCCCC	CNTCAAACCC	CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT	CCTACTGACC	TGTGCTTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCTT	360
GNGGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAATCATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCCTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGCA	TNATGAATCN	GCCAACCCCC	GGGGAAAAGC	GTTTGCGTTT	TGGGCGCTCT	720
TCCGCTTCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTC	CGGCTGCNGC	AAACCGGTTC	780
ACCNCCTCCA	AAGGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTTAAT	GCATCCAAAG	TACTAACAAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTTGGT	TTTCATAAGA	TAATTTATAG	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTTGGCA TAAACAATAA TAAAAAATC ACAATTTAAT AAATAACAAA TACAACATIG 300  
 TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG 350  
 AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTCAC TCAGCCCTGA 420  
 CATTAGTTT TCAAAGTAGG AGACAGGTTT TACAGTATCA TTTTACAGTT TCCAACACAT 480  
 TGAACAACAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA 540  
 TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTTGGTGTGC 600  
 TTATTTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT 660  
 GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTTGA ACTGGAACAT 720  
 TGNATNACAG TGTTCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA 780  
 TGTATTTTTG TTAATAATTA AATTTTAACC TGGTGGAAAA ATAATTTGAA ATNA 834

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT AAGACCTCA TCAATAGATG GAGACATACA GAAATAGTCA 60  
 AACCACATCT ACAAATGCC AGTATCAGGC GCGGCTTCG AAGCCAAAGT GATGTTTGGA 120  
 TGTAAGTGA AATATTAGTT GCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT 180  
 GACGTGAAGT CCGTGAAGC CTGTGGCTAC AAAAAATGTT GAGCCGTAGA TGCCGTCCGA 240  
 AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAGG AGGGTAAAAT AGAGACCCAG 300  
 TAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG 360  
 GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC 420  
 TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TGGGGGCCAG TGCCCTCCTA GTTGGGGGGT 480  
 AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA 540  
 GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTTGG ACAGGTGGTG TGTGGTGGCC 600  
 TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTGGG 660  
 TTANTANGGC CTANTATGAA GAACTTTTGG ANTGAATTA AATCAATNGC TTGGCCGGAA 720  
 GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTTA CCCNACCCAT 780  
 GGAATNCNCC CCCCAGACNA NTGNATCCCT ATTCTTAA 818

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA 60  
 CGGGCCCTAT TTCAAAGATT TTTAGGGGAA TTAATCTAG GACGATGGGT ATGAAACTGT 120  
 GGTTCGCTCC ACAGATTTCA GAGCATTGAC CGTAGTATAC CCCCAGTCTG GTAGCGGTGA 180  
 AAGTGGTTTG GTTTAGACGT CCGGGAATTG CATCTGTTT TAAGCCTAAT GTGGGGACAG 240  
 CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGGCT TCAATCGGGA 300

GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG 360  
 GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC 420  
 ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGATCGT TGAATCGTC TGTATGTAA 480  
 AGGATNCCCT NGGGATGGGA AGGCNATNAA GGAATANGGA TNAATGGCGG GCANGATATT 540  
 TCAAACNGTC TCTANTTCCT GAAACGTCTG AAATGTTAAT AANAATTAAN TTTNGTTATT 600  
 GAATNTTNGG GAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNTAANGG 660  
 CNTTATCNTN AAAGGTNATA ACCNCTCCTA TNATCCCAAC CAATNGNATT CCCCACNCNN 720  
 ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCNC CTTTGTTC 780  
 CTTNANTGAN GGTTATTCNC CCCTNGCNTT ATCANCC 817

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAACC TGCTAACGTG GGAATCGGTG 60  
 CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGACAAGC GGGAGAGCGA CTCCGAGCGT 120  
 CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG 180  
 TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCTGGGG 240  
 TGGGTGGCCG ANGCTTGANC CGCTCTGCCT TGCTGCCCCC ANGTGGGCGG CCACCCCTG 300  
 ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCCACANGG 360  
 GGATTTTGCT CCTANANTAA GGCTCATCTG GGCCTCGGCC CCCCACCTG GTTGGCCTTG 420  
 TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTENG GACCACCTTT NGGGAGTGT 480  
 CTCCTTACAA CCACANNATG CCCGGCTCCT CCGGAAACC ANTCCCANCC TGNAAAGGAT 540  
 CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGGAAAC CNCCTTNTGT 600  
 TCCTTTTNT TNAGGGTTAA TNNCGCCTTG GCCTTNCAN NGTCTNCNC NTTTTCCNNT 660  
 GTTNAATTTG TTANGCNCCC NCCNNTCCCN CNNCNCCAN CCGGACCCNN ANNTTNANN 720  
 NCCTGGGGGT NCCNNGCAT TGACCCNCC NCCCTNTANT TGCNTTNGGG NNCNNTGCC 780  
 CTTTCCCTCT NGGGANCCG 799

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTTG 60  
 TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGCCCA GATGGACATG GGGCTCACT 120  
 CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCACAT GATCCTTACT CTATGAGCAA 180  
 AATCCCCTGT GGGGGCTTCT CTTGAAGTC CGCCANAGG GTCAGTCTT TGGACCCANG 240  
 CAGGTCATGG GGTGTNGNC CAACTGGGGG CCNCAACGCA AAANGGCNCA GGGCCTCNGN 300  
 CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGCGCTG 360

TTCNTACCCG CGNATNTGTC CCANCTGTTT CNGTGCCNAC TCCANCTTCT NGGACGTGCG 420  
 CTACATACGC CCGGANTCNC NCTCCCGCTT TGTCCCTATC CACGTNCCAN CAACAAATTT 480  
 CNCCNTANTG CACCNATTCC CACHTTTTNNC AGNTTTCNC NCGNGCTTC CTNTTAAAAG 540  
 GGTGAGNCCC CGGAAAATNC CCCAAAGGGG GGGGGCCNGG TACCCAACTN CCCCCTNATA 600  
 GCTGAANTCC CCATNACCNN GNCTCNATGG ANCCNTCCNT TTAANNACN TTCTNAACTT 660  
 GGGAAANACC CTCGNCCNTN CCCCCTTAA TCCCNCTTG CNANGNNCNT CCCCNTTCC 720  
 NCCCNNTNG GCNTNTNANN CNAAAAAGGC CCNMANCAA TCTCCTNNCN CCTCANTTCG 780  
 CCANCCCTCG AAATCGGCCN C 801

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 789 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC 60  
 ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCTCACCAGG GTTCACCTTC TCAGCCCTGC 120  
 AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TTCCTGCCCA 180  
 AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCTGC 240  
 CAGGCCCTAA GCCTGGAGCT CCCTTCCTTA ATGGACACGT GGGTGTGGA GGCAGTGGCC 300  
 TGCTCCCACC TCCACCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG 360  
 TGGTGGGTGA GCCACCGAN GCCAGGTGG ETCCGGGCGG GGGCATCTGC CTGGACCTCG 420  
 CCATCCTGGA TAGTGCTTCC TGCTGTCCCA NGTGGCCCCA TCCCTGTTTA TGGGCTCCAT 480  
 TGTCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCCGCAGGCC TGGGTCTGGT 540  
 CCCATTTACT TTGCTACACA GGTANTATTT GACAAGAACG ANTTGGCCAA ATACTCAGCG 600  
 TTAATAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC 660  
 TCCTGTTAAC CCCATGGGGC TGCCGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT 720  
 GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG 780  
 GNGTTCCC 789

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 772 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC 60  
 TTTGTAAAT AAATAAGTTA AATATTTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG 120  
 ACCAACAGGC CACATCCTGA TAAAAGGTAA GAGGGGGGTG GATCAGCAA AAGACAGTGC 180  
 TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTA GGA CTCTTCC CCTACAAATA 240  
 ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAACTCC CATGCAAGAG 300  
 CTACATTAAA CGAAGCTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT 360  
 TATTCACTC CCAAAAACCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTTAACC 420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTTAACAGGA	ANCNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCNCCAC	CCNAATNTT	GCTGGGAAAT	TTTTCTCCC	CTAAATNTT	TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAAATGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTGAG	GGAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGC3ACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGCN	TNGTGGCTCC	TGTTCAAGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANNC	G			751

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 729 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTTCAGA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCAATTT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAA	GGCTGAGCAC	TTCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAAC	TACGGATTTT	600

GAAGANTCAC CTACTTCAAA GAAAANAGTG CCTTTCCCCC-ATTTCTGTTG CAATTGACAA 660  
ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAACCC AAANGGGTCC CCAACCANAA 720  
ATTNAAGGG 729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG 60  
TGTTGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGACAGG TCCTGTGTCT 120  
GGCAGGTCCA CGCAGTGCCC TTTGTCACCT GGGAAATGGA TGCGCTGGAG CTCGTCAAAG 180  
CCACTCGTGT ATTTTTCACA GGCAGCCTCG TCCGACGCGT CGGGGCGAGTT GGGGGTGTCT 240  
TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAAGTGG GGTGGGCTGA 300  
CANGTGCCAG AGCACACTGG ATGGCGCCTT TCCATGNNAN GGGCCCTGNG GGAAAGTCCC 360  
TGANCCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACA CCCCACAGG CTAGAATGGA 420  
ATCTTCTTCC CGAAAGGTAG TTNTTCTTGT TGCCCAANCC ANCCCCNTAA ACAAACTCTT 480  
GCANATCTGC TCCGNGGGGG TCNTANTACC ANCGTGGGAA AAGAACCCCA GCGNGCGAAC 540  
CAANCTGTT TGGATNCGAA GCNATAATCT NCTNTTCTG TTGGTGGACA GCACCANTNA 600  
CTGTNNANCT TTAGNCCNTG GTCCTCTGTT GTTGNNCTTG AACCTAATCN CCNNTCAACT 660  
GGGACAAGGT AANTNGCCNT CTTTNAATT CCNANCTTN CCCCCTGGTT TGGGGTTTTN 720  
CNCNCTCCTA CCCCAGAAAN NCCGTGTTCC CCCCCAATA GGGGCCNAAA CCNNTTNTTC 780  
CACAACCCIN CCCCACCCAC GGGTTCNGNT GGTTCNG 816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG 60  
ATGTGGAAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG GTAGAGAGGA 120  
AAGACCCAAA CCAGGTGGAA CTGTGGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA 180  
CAGTGACTAG CTCAGACCAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA 240  
CCAAGCAGAC AGAAGACTAC TGCCTCGCAT CCAACAANGT GGGTCGCTGC CGGGGCTCTT 300  
TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAE GAGTTTCGTT TATGGAGGCT 360  
GCTTGGGCAA CAAGAACAAC TACCTTCGGG AAGAAGAGTG CATTCTANCC TGTGNGGGTG 420  
TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCCCT 480  
CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCCGCTGCA 540  
NCAATGGCTG CTGCATCNAC ANTTTCTCTG AATTGTGACA ACACCCCCCA NTGCCCCCAA 600  
CCCTCCCAAC AAAGCTTCCC TGTTNAAAAA TACNCCANTT GGCTTTTAC AAACNCCCGG 660  
CNCCTCCNTT TTCCCCNNTN AACAAAGGGC NCTNGCNTT GAACTGCCCN AACCCNGGAA 720

TCTNCCNNGG AAAAANTNCC CCCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC  
CCC

780  
783

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCCACTTGT	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAOGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAAA	GACCACAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCCACTGC	600
CNACAGGGCT	GCNCCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAACTGAAA	CCNTGCATGG	TGGCCCTGT	TCAGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCCN	G				801

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 740 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCGTC	CAGTGCCATG	CAGTTTGTCA	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCTTGGGCT	GCTATGGTGC	360
TAAGACGGAG	AGCAAGTGTG	CCCTCGTGAC	GTTCTTCTTC	ATCCTCCTCC	TCATCTTCAT	420
TGCTGAAGTT	GCAGCTGCTG	TGGTCGCCTT	GGTGTACACC	ACAATGGCTG	AACCATTCCT	480
GACGTTGCTG	GTANTGCCTG	CCATCAANAA	AGATTATGGG	TTCCCAGGAA	AAATTCACCT	540
AANTNTGGAA	CACCNCCATG	AAAAGGGCTC	CAATTTCTGN	TGGCTTCCCC	AACTATACCG	600
GAATTTTGAA	AGANTCNCCC	TACTTCCAAA	AAAAAANANT	TGCCTTTNCC	CCCNCTTCTGT	660
TGCAATGAAA	ACNTCCCAAN	ACNGCCAATN	AAAACCTGCC	CNNNCAAAAA	GGNTCNCAAA	720
CAAAAAAANT	NNAAGGGTTN					740



## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA      60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG      120
GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT      180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCACTAA GTAGTCAGCG TATGTCCCAT      240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA      300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT      360
GGATGAGTGT GGCCAGCGCT GCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT      420
GGTTCTGCCC TGTCACTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG      480
GCTCAGGATG TCCAGAGACG TGGTTCGGCC CCCTCNCCTA ATGACACCGN CCANCAACC      540
GTCGGCTCCC GCCGANTGNG TTCGTCTGTC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC      600
AANCTTCGTC NGGCCCATGG AATTCAACNC ACCGGAACNT GTANGATCCA CTNNTTCTAT      660
AACCGGNCGC CACCGCNCNT GGAACCTCAC TCTTNTTNC TTTACTTGAG GGITAAGGTC      720
ACCTTNNCG TTACCTTGGT CCAAAGCNTN CCNTGTGTG ANATNGTNA TCNGGNCNA      780
TNCCANCCNC ATANGAAGCC NG          802

```

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG      60
GAGCCCACCG TCACNGGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT      120
CNTGACCCCA ACTCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG      180
CAGGAACCAA GANCAAANNC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC      240
GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCTACT TGTTTGGAGA ACNGCNCNNGA      300
CATGCCCAGN GTTANATAAC NGGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGCGCAN      360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCCT      420
CCACTAAGCT CAGAACAAAA AACTTCGACA CCACCTCANTT GTCACCTGNC TGCTCAAGTA      480
AAGTGTAACC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCCTGG      540
GAAGACCTAT CAATTNAAGC TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC      600
CNCNNTCCA AGGGGGGGNC GGCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCCN      660
CCCCNGGCC CGGCTTTTA CNANCNTCNN NNACNGGGNA AAACCNNGC TTTNCCCAAC      720
NNAATCCNCC T          731

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC      60
CAACCCCTC NTCCAAATNN CCNTTCCGG GNGGGGGTTC CAAACCCAAN TTANNTTGG      120
ANNTTAAATT AAATNTTNNNT TCGNGGNNA ANCCNAATGT NANGAAAGTT NAACCCANTA      180
TNANCTTNA TNCCTGAAA CCNGTNGNTT CAAAAAATNT TTAACCTTA ANTCCCTCCG      240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTTGTTT GAAGGNTNAA TNAAAANCCC      300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTTCC NTTAAAANAA      360
GGNNANCCCC GGTANTNAA TCCCCCNCC CCAATTATA CCGANTTTT TTNGAATTGG      420
GANCCNCGG GAATTAACGG GGNNTTCCC TTTGGGGGG CNGGNCCCC CCCNTCGGG      480
GGTTNGGGNC AGGNCNNAAT TGTTTAAGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC      540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCC CANGGCCCTT CCGNANAGT TGGGGTTGG      600
GGGGCCTGGG ATTTTNTTTC CCCTNTNCC TCCCCCCCC CNGGGANAG AGGTTNGNT      660
TTTGNTCNCN GGGCCCNCCN AAGANCTTN CCGANTTNAN TTAAATCCNT GCCTNGGCCA      720
AGTCCNTTGN AGGGNTAAAN GGCCCCCTNN CGGG      754

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

ATCANCCCAT GACCCNAAC NNGGGACCNC TCANCCGGNC MNNCNACCNC CGGCCNATCA      60
NNGTNAGNNC ACTNCNNTN NATCACNCCC CNCCNACTAC GCCCNANANC CNACGCNCTA      120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCANACN      180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN      240
NNCNANANAT GATTTTCCTN ANCCGATTAC CCNTNCCCCC TANCCCCCTC CCCCCAACNA      300
CGAAGGCNCT GGNCCNAAGG NNGCGNCNCC CCGCTAGNTC CCCNNCAAGT CNCNCNCCTA      360
AACTCANCCN NATTACNCGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC      420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT      480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATTT CCNAANGGCT      540
CTTTCNGACA GCATNTTTTG GTTCCNNTT GGGTCTTAN NGAATTGCCC TTCNTNGAAC      600
GGGCTCNTCT TTTCCTTCGG TTANCTGGN TTCNNCCGGC CAGTTATTAT TTCCCNTTTT      660
AAATTCNTNC CNTTTANTTT TGGCNTTCA AACCCCCGGC CTTGAAAACG GCCCCCTGGT      720
AAAAGGTTGT TTTGANAAAA TTTTGTGTTT GTTCC      755

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

TTTTTTTTTT TTTTANGTG TNGTCGTGCA GGTAGAGGCT TACTACAANT GTGAANACGT 60
ACGCTNGGAN TAANGCGACC CGANTTCTAG GANNCCNCCCT AAAATCANAC TGTGAAGATN 120
ATCCTGNNNA CGGAANGGTC ACCGGNNGAT NNTGCTAGGG TGNCNCTCC CANNNCNTTN 180
CATAACTCNG NGGCCCTGCC CACCACCTTC GGCGGCCCN NGNCCGGGCC CGGGTCATTN 240
GNNTTAACCN CACTNNGCNA NCGGTTTCCN NCCCNCCNG ACCCNGGCCA TCCGGGGTNC 300
TCTGTCTTCC CCTGNAGCN ANAAANTGGG CCNCGGNCCC CTTTACCCCT NNACAAGCCA 360
CNGCCNTCTA NCCNCGCCC CCCCTCCANT NNGGGGGA CTTCNANNGCT CCGTTNCTNG 420
NNACCCCN NN GGTNCCTCG GTTGTGANT CNACCGNANG CCANGGATT CNAAGGAAGG 480
TGCGTTNTTG GCCCTACCC TCGCTNCGG NNCACCTTC CCGACNANGA NCCGCTCCCG 540
CNCNCGMNG CCTCNCCTCG CAACACCCGC NCTCNTNGT NCGGNNNCCC CCCACCCGC 600
NCCCTCNC NCNGCNANCN CTCCNCCNCC GTCTCANNCA CCACCCCGCC CCGCCAGGCC 660
NTCANCCACN GGNAGACNNG NAGCNCNNTC GCNCCGCGCN GCGNCCCT CGCCNCGAA 720
CTNCNTCNGG CCANTNCGC TCAANCCNNA CNAACGCCG CTGCGCGGCC CGNAGCGNCC 780
NCCTCCNCGA GTCCTCCCGN CTTCCNACCC ANGNNTTCN CGAGGACACN NNACCCCGCC 840
NCCANGCGG 849
  
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

GCGCAAATA TACTTCGCTC GNACTCGTGC GCCTCGCTNC TCTTTTCCTC CGCAACCATG 60
TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCCAAACT GANTAACACA 120
CACACNCNAN AGANAAATCC NCTGGCTTCC ANAGTANACN ATTGAACNNG AGAACCANGC 180
NGGCGAATCG TAATNAGGCG TGCGCCGCCA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC 240
CTNCCNACCC TACNTCTCN NAGCTGTCNN ACCCCTNGTN CGNACCCCCC NAGGTGGGA 300
TCGGGTTTNN NNTGACCGNG CNCCCCCTCC CCCCTCCAT NACGANCCNC CCGCACCACC 360
NANNGCNC GC NCCCCGNCT CTGCGCCNCC CTGTCTNTN CCCCTGTNGC CTGGCNCNGN 420
ACCGCATTGA CCCTCGCCNN CTNCNNGAAA NCGNANACGT CCGGGTTGNN ANNANCGCTG 480
TGGGNNNGCG TCTGCNCCGC GTTCCTTCN NCNCTTCCA CCATCTTCNT TACNGGGTCT 540
CCNCGCNTC TCNNACACNC CCTGGGACGC TNCCTNTGC CCCCCTTNA TCCCCCCTT 600
CGNCGTGNCC CGNCCCCACC NTCATTNCA NACGNTCTTC ACAANNCCCT GGNTNNCTCC 660
CNANCNGCN GTCANCCNAG GGAAGGGNGG GGNNCCNNTG NTTGACGTTG NGGNGANGTC 720
CGAANANTCC TCNCCNTCAN CNCTACCCCT CGGGCGNNT CTGNGTNC AACTTANCAA 780
NTCTCCCCG NGNCNNTC TCAGCCTCNC CCNCCCNCT CTCTGCANTG TNCTCTGCTC 840
TNACCNTAC GANTNTTCGN CNCCCTCTTT CC 872
  
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA	60
NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNNGTA	120
TCNTNCATTA GTAACAANTG TNNTGTCCAT CCTGTCTNGAN CANATTCCCA TNNATTNCGN	180
CGCATTTCNCN GCNCANTATN TAATNGGGAA NTCNNNTNNN NCACCNNCAT CTATCNTNCC	240
GCNCCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN	300
AANANCCCC CGCNGNCCAC CGGTNGNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT	360
AACCTGCGTC AGANNATCA AACNTGGGAA ACCCGCNNCC ANGTNNAAGT NGNNNCANAN	420
GATCCCGTCC AGGNTTNACC ATCCCTTCNC AGCGCCCCCT TTNGTGCCTT ANAGNGNAGC	480
GTGTCCNANC CNCTCAACAT GANACGCGCC AGNCCANCCG CAATTNGGCA CAATGTCGNC	540
GAACCCCTA GGGGGANTNA TNCAAANCC CAGGATTGTC CNCNCANGAA ATCCCNCAAC	600
CCCNCCCTAC CCNNCTTTGG GACNGTGACC AANTCCCGGA GTNCCAGTCC GGCCNGNCTC	660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCGAGGN NTCGNAAGGA	720
ACCGGNCCTN GGNCGAANNG ANCNNTCNGA AGNGCCNCNT CGTATAACCC CCCCTCNCCA	780
NCCNACNGNT AGNTCCCCC CNGGGTNCGG AANGG	815

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG	60
AGGCTATCCA GCGTACTCCA AAGATTCAGG TTTACTCAGC TCATCCAGCA GAGAAATGGAA	120
AGTCAAATTT CCTGAATTGC TATGTGTCTG GGTTCATCC ATCCGACATT GAANTTGACT	180
TACTGAAGAA TGGANAGAGA ATTGAAAAG TGGAGCATT AGACTTGTCT TTCAGCAAGG	240
ACTGGTCTT CTATCTCNTG TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG	300
CCTGCCGTGT GAACCATGTG ACTTTGTCAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTTGAAGAT GCCGCATTG GATTGGATGA ATTCCAAATT	420
CTGCTTGCTT GCNTTTTAAT ANTGATATGC NTATACACCC TACCCTTTAT GNCCCCAAAT	480
TGTAGGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCCNTTCG	540
AATTGCCCCG CNCCNGTTN NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTCNCC	600
TCTTACGGAA GGGCCTGGGC CNCTTTNCAA GGTGGGGGA ACCNAAAATT TCNCTTNTGC	660
CCNCCNCCA CNNTCTTGNG NNCNCANTTT GGAACCTTC CNATTCCCCCT TGGCCTCNNA	720
NCCTTNNCTA ANAAACTTN AAANCGTNGC NAAANNTTN ACTTCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
ANATTANTAC AGTGTAACTCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT 60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC ATTTCCTGCA 120
GAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCCAGAG GGGTGAGTAG 180
CCATCANGCC TTCGGTEGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA 240
NTGATGACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA 300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC 360
TTCCTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCNCCTG GGANCAGCTA 420
ACNNAGCACT CACCTGCCCC CCCATGGCCG TNCGNCCTCC TGGTCCTGNC AAGGGAAGCT 480
CCCTGTTGGA ATTNCGGGGA NACCAAGGGA NCCCCCTCCT CCANCTGTGA AGGAAAAANN 540
GATGGAATTT TNCCTTCCG GCCNNTCCCC TCTTCCTTTA CACGCCCCCT NNTACTGNTC 600
TCCCTCTNTT NTCCTGNCNC ACTTTTNACC CCNNNATTTT CCTTNATTGA TCGGANNCTN 660
GANATTCCAC TNNCCCTTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGGAT 720
GGGNNCCTCG NTCATCCTCT CTTTTTCNCT ACCNCCNNTT CTTTGCCTCT CCTTGATCA 780
TCCAACCNCT GNTGGCCNTN CCCCCCNNTT TCCTTTNCCC 820
```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 818 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
TCTGGGTGAT GGCCTCTTCC TCCTCAGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT 60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTCAGCCCT GCCCAACCTG ATTCTGATGA 120
CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGGCG 180
CTGCTGAGCA CTTCCGCCCC TCACCTGCC CAGCCCCTGC CATGAGCTCT GGGCTGGGTC 240
TCCGCCTCCA GGGTCTGCT CTTCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC 300
TTCTTCCTGC CCCNTCCCTG GCTCTGANTC TGTGTCTTCC TGTCTGTGC ANGNCCTTG 360
GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTCTGANN TCTTCANTTA ACTNTGANTT 420
TATNACCNAN TGGNCTGTNC TGTCNNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC 480
NCTCCCTTCC ANTCNNNNA ACCNGCTTNC ENTCTCTCC CCNTANCCCG CCNGGGAANC 540
CTCCTTTGCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC 600
CTGNTNNCCC CNCTCNCNNT TNCCTCGTCC CNNCNCGCN NNGCANNTTC NCNGTCCCN 660
TNNCTCTCN NGTNTCGNAA NGNTCNCNTN TNNNNNGCN NGNTNNTNCN TCCCTCTCNC 720
CNNNTGNANG TNNTTNNNC NCNGNCCCC NNNNCNNNN NGGNNTNNN TCTNCNCNGC 780
CCCNCCCCC NGNATTAAGG CCTCCNNTCT CCGGCCNC 818
```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 731 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG      60
TCCCAACATG ANGGTGNNGT TCTCTTTTGA ANGAGGGTTG NGTTTTTANN CCNGGTGGGT      120
GATTNAACCC CATGTATGG AGNNAAGGN TTTNAGGGAT TTTTCGGCTC TTATCAGTAT      180
NTANATTCCT GTNAATCGGA AAATNATNTT TCNNCNGGAA AATNTTGCTC CCATCCGNAA      240
ATTNCTCCCG GGTAGTGCAT NTTNGGGGNG CNGCCANGTT TCCCAGGCTG CTANAATCGT      300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG      360
TNNNTTNCCT TCGCCCTNTG ACTCTGCNNG AGCCCAATAC CCNNGNGNAT GTCNCCCNGN      420
NNNGCGNCNC TGAAANNNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAAGCNC      480
CGTTTCNCAT NAAGGCACTT TNGCCTCATC CAACCCTNG CCCTCNCNA TTTNGCCGTC      540
NGGTCNCCT ACGCTNNTNG CNCCTNNNTN GANATTTTNC CCGCCTNGGG NAANCCTCCT      600
GNAATGGGTA GGGNCTTNTC TTTTNACCNN GNGGTNTACT AATCNCCTNC ACGCNTNCTT      660
TCTCNACCCC CCCCCTTTT CAATCCCANC GGCNAATGGG GTCTCCCCNN CGANGGGGGG      720
NNNCCCANNC C

```

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 822 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

ACTAGTCCAG TGTGGTGGA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT      60
CGCTCANACC TCACANCCTC CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNNT      120
ATNTNTACNC TCATANNCTC CNNNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN      180
TNNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC      240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN      300
TCCATNANTT ANNNTAACTA CCACTGACNT NGACTTTCNC ATNANCTCCT AATTGTGAATC      360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC      420
NTCAACAACC TATCTANCTG TTCNCCAACC TTNCCTCCG ATCCCENNAC AACCCCCCTC      480
CCAAATACCC NCCACCTGAC NCCTAACCCN CACCATCCCG GCAAGCCNAN GGNCATTTAN      540
CCACTGGAAT CACNATNGGA NAAAAAACC CCNAACTCTC TANCNCNNAT CTCCCTAANA      600
AATNCTCCTN NAATTTACTN NCANTNCCAT CAANCCACN TGAAACNNA CCCCTGTTTT      660
TANATCCCTT CTTTCGAAA CCNACCCTTT ANNNCCCAAC CTTTNGGGCC CCCCENCTNC      720
CCNAATGAAG GNCNCCCAAT CNANGAACG NCCNTGAAA ANCNAGGCNA ANANNNTCCG      780
CANATCCTAT CCCTTANTTN GGGNCCCTT NCCCNGGGCC CC

```

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 787 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

CGGCCGCTG CTCTGGCACA TGCCTCCTGA ATGGCATCAA AAGTGATGGA CTGCCCATTG 60
CTAGAGAAGA CCTTCTCTCC TACTGTCAAT ATGGAGCCCT GCAGACTGAG GGCTCCCCTT 120
GTCTGCAGGA TTTGATGTCT GAAGTCGTGG AGTGTGGCTT GGAGCTCCTC ATCTACATNA 180
GCTGGAAGCC CTGGAGGGCC TCTCTCGCCA GCCTCCCCCT TCTCTCCACG CTCTCCANGG 240
ACACCAGGGG CTCCAGGCAG CCCATTATTC CCAGNANGAC ATGGTGTTTC TCCACGCGGA 300
CCCATGGGGC CTGNAAGGCC AGGGTCTCCT TTGACACCAT CTCTCCCGTC CTGCCTGGCA 360
GGCCGTGGGA TCCACTANTT CTANAACGGN CGCCACCNCG GTGGGAGCTC CAGCTTTTGT 420
TCCCNNTAAT GAAGGTTAAT TGCNCGCTTG GCGTAATCAT NGGTCANAAC TTTTCTCTGT 480
GTGAAATTGT TTNTCCCTC NCNATTCNC NCNACATAAC AACC CGGAAN CATAAAGTGT 540
TAAAGCCTGG GGGTNGCCTN NGAATNAAC TNAACTCAAT TAATTGCGTT GGCTCATGGC 600
CCGCTTTCCN TTCNGGAAAA CTGTCNTCCC CTGCNTTNNT GAATCGGCCA CCCCCNNGG 660
AAAAGCGGTT TGCNTTTTNG GGGGNTCCTT CCNCTTCCCC CCTCNCTAAN CCTNCGCCT 720
CGGTCGTTNC NGGTNGCGGG GAANGGNGAT NNNCTCCCC NAAGGGGGNG AGNNNGNTAT 780
CCCCAA 787

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

TTTTTTTTTT TTTTTTTGGC GATGCTACTG TTAATTGCA GGAGGTGGGG GTGTGTGTAC 60
CATGTACCAG GGCTATTAGA AGCAAGAAGG AAGGAGGGAG GGCAGAGCGC CCTGCTGAGC 120
AACAAAGGAC TCCTGCAGCC TTCTCTGTCT GTCTCTTGGC GCAGGCACAT GGGGAGGCCT 180
CCCGCAGGGT GGGGGCCACC AGTCCAGGGG TGGGAGCACT ACANGGGGTG GGAGTGGGTG 240
GTGGCTGGTN CNAATGGCCT GNCACANATC CTAAGATTTC TTGACACCTG GATTTCACCA 300
GGGGACCTTC TGTTCTCCCA NGGNAACTTC NNNATCTCN AAAGAACACA ACTGTTTCTT 360
CNGCANTTCT GGCTGTTTAT GGAAAGCACA GGTGTCCNAT TTNGGCTGGG ACTTGGTACA 420
TATGGTTCGG GCCCACCTCT CCCNTCNAAN AAGTAATTCA CCCCCCCCN CCNTCTNTTG 480
CCTGGGGCCT TAANTACCA CACCGGAAC CANTTANTTA TTCATCTTNG GNTGGGCTTG 540
NTNATCNCCN CCTGAANGCG CCAAGTTGAA AGGCCACGUC GTNCCCNCTC CCCATAGNAN 600
NTTTTNNCNT CANCTAATGC CCCCCCNGG AACNATCCAA TCCCCCCCN TGGGGGCCCC 660
AGCCCANGGC CCCCNGCTCG GGNNNCCNGN CNCGNANTCC CCAGGNTCTC CCANTCNGNC 720
CCNNNGCNCC CCCGCACGCA GAACANAAGG NTNGAGCCNC CGCANNNNNN NGGINNCCNAC 780
CTCGCCCCCC CCNNCGNNG 799

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTTNCNAG	GGCAGGTTTA	TGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGCGCGCG	GCGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTIN	AATTTCACG	GGCACAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCCG	TTGGCNCAC	CCCCNTGGAA	ACCAC'TNNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	CAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TINNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAAACNC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNACGNC	TANCAANGNA	TCCCTTTTTT	TANAAACGGG	780
CCCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCC	GCCATCCCTT	CTTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCNCCTCCC	GCTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GCCGCGACCG GCATGTACGA GCAACTCAAG GCGGAGTGGA ACCGTAAAAG CCCCAATCTT      60
ANCAAGTGCG GGGGAANAGCT GGGTCGACTC AAGCTAGTTC TTCTGGAGCT CAACTTCTTG      120
CCAACCACAG GGACCAAGCT GACCAAACAG CAGCTAATTC TGGCCCGTGA CATACTGGAG      180
ATCGGGGGCCC AATGGAGCAT CCTACGCAAN GACATCCCCT ECTTCGAGCG CTACATGGCC      240
CAGCTCAAAT GCTACTACTT TGATTACAAN GAGCAGCTCC CCGAGTCAGC CTATATGCAC      300
CAGCTCTTGG GCCTCAACCT CCTCTTCCTG CTGTCCCAGA ACCGGGTGGC TGANTNCCAC      360
ACGGANTTGG ANCGGCTGCC TGCCCAANGA CACACANACC AATGTCTACA TCNACCACCA      420
GTGTCCTGGA GCAATACTGA TGGANGGCAG CTACCNCAAA GTNTTCCTGG CCNAGGGTAA      480
CATCCCCCGC CGAGAGCTAC ACCTTCTTCA TTGACATCCT GCTCGACACT ATCAGGGGATG      540
AAAAATCGCNG GGTGCTCCA GAAAGGCTNC AANAANATCC TTTTCNCTGA AGGCCCCCGG      600
ATNCTNCTAGT NCTAGAATCG GCCCGCCATC GCGGTGGANC CTCCAACCTT TCGTTNCCCT      660
TTACTGAGGG TTNATTGCCG CCCTTGGCGT TATCATGGTC ACNCCNGTTN CCTGTGTTGA      720
AATTNTTAAC CCCCCACAAT TCCACGCCNA CATTTG      756

```

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GGGGATCTCT ANATCNACCT GNATGCATGG TTGTCGGTGT GGTGCTGTC GATGAANATG      60
AACAGGATCT TGCCCTTGAA GCTCTCGGCT GCTGTNTTTA AGTTGCTCAG TCTGCCGTCA      120
TAGTCAGACA CNCTCTTGGG CAAAAAACAN CAGGATNTGA GTCTTGATT CACCTCCAAT      180
AATCTTCNGG GCTGTCTGCT CCGGTGAATC GATGACNANG GGCAGCTGGT TGTGTNTGAT      240
AAANTCCANC ANGTTCTCCT TGGTGACCTC CCCTTCAAAG TTGTTCCGGC CTTTCATCAA      300
CTTCTNNAAN ANGANNANCC CANCTTTGTC GAGCTGGNAT TTGGANAACA CGTCACTGTT      360
GGAAACTGAT CCCAAATGGT ATGTCATCCA TCGCCTCTGC TGCCTGCAAA AAAGTTGCTT      420
GGCNCAAATC CGACTCCCN TCCTTGAAAG AAGCCNATCA CACCCCCCTC CCTGGACTCC      480
NNCAANGACT CTNCCGCTNC CCCNTCCNNG CAGGGTTGGT GGCANNCCGG GCCCNTGCGC      540
TTCTTCAGCC AGTTACACAT NTTCATCAGC CCTCTGCCA GCTGTTNTAT TCCTTGGGGG      600
GGAANCCGTC TCTCCCTTCC TGAANNAACT TTGACCGTNG GAATAGCCGC GCNTCNCCNT      660
ACNTNCTGGG CCGGGTTCAA ANTCCCTCCN TTGNCCNNTCN CCTCGGGCCA TTCTGGATT      720
NCCNAACTTT TTCTTCCCC CNCCCCNCGG NGTTTGGNTT TTTCATNGGG CCCCCAATCT      780
GCTNTTGGCC ANTCCCTTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNTNG GGCC      834

```

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTGA	180
GGAAAGGCTT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTTT	GTTCTCATGG	CTGCCCACCG	CAGCCTGGCA	300
CTAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGATCG	TATCACTGCC	ACNTTTCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTGTG	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCTT	GGGTCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAA	TGANATCCCC	NGAAGCACCC	TNCCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCACTGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGTAGTAC	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCTT	120
GTGCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTGATN	CANCAGCCCA	TGCTGCAGC	GGAAGTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAACTGCCT	CTCAAAGGCC	ACCTTGACCA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCAATNN	TACCANGGTT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNGTTC	CNCTNNGGTG	GTCTGAAACT	AATCACCCTC	660
ACTGGAAAAA	GGTANGTGCC	TTCCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAAT	TGTCCAACCC	CCTCANNCAA	ATNNCCATT	CCGGGGGGGG	GTTCCAAACC	120

CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA 180  
 AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTTTAAACC 240  
 CTAAATCCC TCCGAAATTG NTAANGGAAA ACCAAATTCN CCTAAGGCTN TTTGAAGGTT 300  
 NGATTTAAAC CCCCTTNANT TTTTTTNACC CNNGNCTNAA NTATTNGNT TCCGGTGTTC 360  
 TCCTNTTAAN CNTNGGTAAC TCCCNTAAT GAANNCCCT AANCCAATTA AACCGAATTT 420  
 TTTTGAATT GGAAATCCN NGGAATTNA CCGGGGTTTT TCCNTTTGG GGGCCATNCC 480  
 CCCNCTTTCG GGGTTTGGGN NTAGGTGAA TTTTNNANG NCCCAAAAAA NCCCCAANA 540  
 AAAAACTCC CAAGNNTTAA TTNGAATNTC CCCCTTCCA GGCCTTTTGG GAAAGGNGGG 600  
 TTTNTGGGGG CCNGGGANTT CNTTCCCCCN TTNCCNCCCC CCCCCNGGT AAANGGTTAT 660  
 NGNNTTGGT TTTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAAT CCCCAGGNGC 720  
 GCCG 724

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTCTTTG CTCACATTTA ATTTTATTT TGATTTTTTT TAATGCTGCA 60  
 CAACACAATA TTTATTTTAT TTGTTTCTTT TATTTTCAATT TATTTGTTTG CTGCTGCTGT 120  
 TTTATTTTATT TTTACTGAAA GTGAGAGGA ACTTTTGTGG CCTTTTTTCC TTTTCTGTGA 180  
 GGCCGCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT 240  
 CGAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTTGTAA TCATGCCCTA TGGTGGGTGA 300  
 TTAAGTCTT GTACAATTAC NTTTCACTTT TAATTAATTG TGCTNAANGC TTTAATTANA 360  
 CTTGGGGGTT CCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG 420  
 TCCCGGCNNT CNTTGAAACA CACNGCNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAAA 480  
 TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCNNN GCCTGAATCC TCNAAAANCN 540  
 CCCTCAANCN AATTNCTNNG CCCCGGTGNC GCNTNNGTCC CNCCCGGGCT CCGGGAANTN 600  
 CACCCCNCA ANNCNNTNNC NAACNAAAT CCGAAAATAT TCCCNNTCNC TCAATTCCCC 660  
 CNNAGACTNT CCTCNNGNAN CNCAATTTTC TTTNNTCAC GAACNCGNNC CNNAAAATGN 720  
 NNNNCNCTC CNCTNGTCCN NAATCNCCAN C 751

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT CTGTAAGATC AGGTGTTCTT CCCTCGTAGG TTTAGAGGAA ACACCCTCAT 60  
 AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG 120  
 CGCCCTATGC ACAGCTGGGC CTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA 180  
 TGGTCTGGAA GCGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAAT 240  
 TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGGT 300

CGGTCATAAN	CGCGGTGGCG	TCGTCGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGGNA	360
ATAAAAGGTG	CGCCCCCGCA	CCGTTCANCT	CGCACTTCTC	NAANACCATG	ANGTTGGGCT	420
CNAACCCACC	ACCANNCCGG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTTGGGC	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCCNNG	ATGCCAANCA	NCCCCAANCC	CCGGGGTCTT	540
AAANCACCCN	CCTCCTCNTT	TCATCTGGGT	TNTTNTCCCC	GGACCNTGGT	TCCTCTCAAG	600
GGANCCCAT	TCTCNACCAN	TACTCACCN	NCCCCCCNT	GNNACCCANC	CTTCTANNGN	660
TTCCCNCCCG	NCCTCTGGCC	CNTCAAANAN	GCTTNCACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCCTATCT	GNACCCCN	TTTGTCTCAN	TNT			753

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATTT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTTCCAC	120
TTCTTTAAAC	CTTGTTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTTTAA	AAAATATCAT	TTGAGAATAT	TCTTTCAGAG	GTATTTTCAT	300
TTTACTTTT	TGATTAATTG	TGTTTTATAT	ATTAGGGTAG	T		341

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTCACAAAC	TTCTAAATAA	ATAATTTTCA	GTGGCTTCAT	A		101

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC 60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT 120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA 180
CCTCTTGAGA GGTCAGTAAA GAGGACTTAA TATTTTCATAT CTACAAAATG ACCACAGGAT 240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC 300
TCGAA 305

```

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTTTCT 60
GATTATTTGG TGTGTGTTT GGTGTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT 120
CTCTCCATCC TCGGGCATT CTTCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT 180
CCAGAATTTT TCTTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC 240
TGCTGTGTGT CTTCTTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA 300
AGACGCCCTC AGATCGGTCT TCCCATTTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA 360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC 420
ACTTGGCAGG GGGGTCTTGC TCCTTTTTC TATCAGGTGA CTCTGCAACA GGAAGGTGAC 480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG 540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTT ATGATGGAAG 600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC 660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG 720
CCGCCCGGTT GAACTCCTGC AAATCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAACT 780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTGTGTGTC CAGGAGGTGA TGGAGCCACT 840
CCCACACCTG GT 852

```

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC	CTTGCTCGCT	AACGACCTCA	TGCTCATCAA	GTTGGACGAA	TCCGTGTCCG	60
AGTCTGACAC	CATCCGGAGC	ATCAGCATTG	CTTCGCAGTG	CCCTACCGCG	GGGAACTCTT	120
GCCTCGTTTC	TGGCTGGGGT	CTGCTGGCGA	ACGGCAGAAT	GCCTACCGTG	CTGCAGTGCG	180
TGAACGTGTC	GGTGGTGTCT	GAGGAGGTCT	GCAGTAAGCT	CTATGACCCG	CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT	TAAATGTTTA	TAAGGCAGAT	CTATGAGAAT	GATAGAAAAC	ATGGTGTGTA	60
ATTTGATAGC	AATATTTTGG	AGATTACAGA	GTTTTAGTAA	TTACCAATTA	CACAGTTAAA	120
AAGAAGATAA	TATATTCCAA	GCANATACAA	AATATCTAAT	GAAAGATCAA	GGCAGGAAAA	180
TGANTATAAC	TAATTGACAA	TGGAAAATCA	ATTTTAATGT	GAATTGCACA	TTATCCTTTA	240
AAAGCTTTCA	AAANAAANAA	TTATTGCAGT	CTANTTAAT	CAAACAGTGT	TAAATGGTAT	300
CAGGATAAAN	AACTGAAGGG	CANAAAGAAT	TAATTTTCAC	TTCATGTAAC	NCACCCANAT	360
TTACAATGGC	TTAAATGCAN	GGAAAAAGCA	GTGGAAGTAG	GGAAGTANTC	AAGGTCTTTC	420
TGGTCTCTAA	TCTGCCTTAC	TCTTTGGGTG	TGGCTTTGAT	CCTCTGGAGA	CAGCTGCCAG	480
GGCTCCTGTT	ATATCCACAA	TCCCAGCAGC	AAGATGAAGG	GATGAAAAAG	GACACATGCT	540
GCCTTCCTTT	GAGGAGACTT	CATCTCACTG	GCCAACACTC	AGTCACATGT		590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC	ATAATGAAGG	AGTGGGGANA	GATTTTAAAG	AAGGAAAAAA	AACGAGGCCC	60
TGAACAGAAT	TTTCTGNAC	AACGGGGCTT	CAAAATAATT	TTCTTGGGGA	GGTTCAAGAC	120

GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG 180  
 CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA 240  
 AACATCAAAG AAAGGAAGGT GCGGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT 300  
 CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCECAGG CTCCTGTGTG 360  
 CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC 420  
 CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCTCTG ACATGGGTGA ACCTCCTATT 480  
 CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC 540  
 ACGGCATGGG AAGCCTTTCT GACTTGCTTG ATTACTCCAG CATCTTGGAA CAATCCCTGA 600  
 TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC 660  
 AGGCTGCTGG CTTCAAATTN TGGCTCATT ACGAGCTATG GGACCTTGGG CAAGTNATCT 720  
 TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAATGG GGGATAATAA TAGT 774

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT 60  
 TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTTT AATTACAGCT CAACGCAACT 120  
 TGGT 124

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT 60  
 TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTTT TACGGGTGAT TGCAAAAATT 120  
 TTAGGGCACC CATATCCCAA GCANTGT 147

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC 60  
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTTGGGA GAGGGGT 107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGACGG 60  
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG 120  
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCC CACTTGGCCA 180  
CCTCCCTTTT GGGACCAGCA ATGT 204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTGATAGTT TTAAAGGTTA GTATTGTGTA 60  
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA 120  
CCATCAGACA GGTTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA 180  
AAAACCTCTT GTATCAATTT CTTTTGTTCA AAATGACTGA CTTAANTATT TTTAAATATT 240  
TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA 300  
ATGTTGCTCA GATAAATAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTTCTGGGGC 360  
ATGCAACAGT GTCTTTTCTT TNCTTTTCTT TTTTTTTTTT TTACAGGCAC AGAAACTCAT 420



CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT 480  
ATCACTCTTG T 491

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTGG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAACACGTT AAAAAAAGT GTTGAAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC	300
AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTCCNCG	420
TANCTTGANT CTGTGTATTC CAGGANCAAG CGGATGGAAT GGGCCAGCCC NCGGATGTTT	480
CANT	484

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA AAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTGTGTTG T	151

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCACGG TCCCCAGAAC GGACACTTTC  
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T

60

91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT  
TGGATTTTTG GSTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC  
AAGGGACAAC TGT

60

120

133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC  
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA  
TCTCANTGGG CTGGATNCAT GCAGGGT

60

120

147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTTATCCT TTAAAAAAGA TGAAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAGTAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCAAAAACCTC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTAATTTCGGC	60
GTCTGGGGCT CCTTCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 154 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT 60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC 120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT 154
```

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
CGCTCGAGCC CTATAGTGAG TCGTATTAGA 30
```

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 89 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
ACAAGTCATT TCAGCACCTT TTGCTCTTCA AAAGTGACCA TCTTTTATAT TTAATGCTTC 60
CTGTATGAAT AAAAATGGTT ATGTCAAGT 89
```

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 97 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG 60  
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT 97

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAACCTT GGAACCCCTT TTTGATGGCA 60  
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC 120  
CCAACCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT 180  
TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA 240  
GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTG GCCGCTGAAC TATGAACCCG 300  
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG 360  
GGGCGGGAGG AGCATGT 377

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG 60

AGAACCCGTG	TGCCCCCTTC	CACCATATCC	ACCCTCGCTC	CATCTTTGAA	CTCAAAGACG	120
AGGAACCTAAC	TGCACCCTGG	TCCTCTCCCC	AGTCCCCAGT	TCACCCTCCA	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCTGAATT	TATGTGTTT	240
TTATATATTT	TTTAATAAGA	TGCACTTTAT	GTCATTTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACTTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTTAAA	AAAGGGGACT	TGCTTAAAAA	AGAAGTCTAG	CCACGATTGT	GTAAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCGTATCTC	AGCACTCCTT	AGTCTGCTTG	300
CCTCTCCAG	GGCCCCAGCC	TGGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTTCT	GTGCTAGTGG	ACCGT				385

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG	ATATATTTTT	ACCCAGATG	GGGATATTCT	TTGTAAAAAA	TGAAAATAAA	60
GTATTTTAA	TGG					73

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGGCCCAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACTT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCAA CTGGACACC TGTGCCTTCC ATGAACAGCC	420
AGAAGTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTCCCT GGGGAGAACA	480
GAANGTCCCT GGGTGAAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACCTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT	180
CCAAAAAGGC CTTCGATACG GGATAATCCT ATTATTACC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCCC AACAGGCATC ACCCCGCTAA ATCCCCTAGA AGTCCCCTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATTT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAAACACA TTTTCTACAT AGATAGTACT 60
AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATT AATATGGTAA GATTGGTTTA 120
TGTGATTTTA GTGGTATTTT TGGCACCTTT ATATATGTTT TCCAAACTTT CAGCAGTGAT 180
ATTATTTCCA TAACTTAAAA AGTGAGTTTG AAAAAGAAAA TCTCCAGCAA GCATCTCATT 240
TAAATAAAGG TTTGTCATCT TTAATAATAC AGCAATATGT GACTTTTTTA AAAAGCTGTC 300
AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA 360
AGTCAGTTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG 420
CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCAATTTTG TATTTTAA AAGTACATGG 480
TAAAAAATAA AATTCACAAC AGTATATAAG GCTGTAAAT GAAGAATTCT GCC 533

```

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA 60
AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA 120
AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG TTGGCTGGAG GAGCTGTGGA 180
AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATTGTT ATTACANAGT 240
GAGGTTCTCT GTGTGCCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA 300
CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAAAC 360
GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCCC GTCTGTTATG 420
ATTTCTCTCC ATTGCAGCNA NAAACCCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA 480
AAATACACCC CCTCTTGAAG NACCNGGAGG A 511

```

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

CAGTGCCAGC ACTGGTGCCA GTACCAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC 60
CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC 120
TGGCCTTGGT GGAGCTGGTG CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTCTCTCTA 180
CAAGTGAGAT TTAGATATT GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC 240

```



CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA 300  
CTCTGCATTA AATCTATTTG CCATTTCTGA AAAAAAAAAA AAAAAAAGG CGGCCGCTCG 360  
ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTGGCAGC 420  
CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCACT 480  
GTCCTTTCCT AANTAAAT

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTT GGATTCAGCC GCGAAGAGAT 60  
TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT 120  
TCCAGGCCCA CGGCTCAAGT GAATTTGAAT ACTGCATTGA CAGTGTAGAG TAACACATAA 180  
CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA 240  
AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG 300  
GGCTTTTGTAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC 360  
CAGTTTGCTT GATATATTTG TTGATATTAA GATTCTTGAC TTATATTTTG AATGGGTTCT 420  
ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTTATTTA CACTCTTGAT 480  
TCTACAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA GTCCCGT 537

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC 60  
TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA 120  
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG 180  
TGGCACAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAAGCGT CTTCTGAGGA 240  
TCTAGTTGGG CTTTCTTTCT GGGTTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA 300  
TCATTATTGT ATAACGGTTT TCAAACNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA 360  
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC 420  
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN 467

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

AAGCTGACAG CATTCTGGGCC GAGATGTCTC GCTCCGTGGC CTTAGCTGTG CTCGCGCTAC      60
TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTCAGGTT TACTCACGTC      120
ATCCAGCAGA GAATGGAAAG TCAAATTTCC TGAATTGCTA TGTGTCTGGG TTTCATCCAT      180
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTGAG      240
ACTTGTCTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA      300
CTGAAAAAGA TGAGTATGCC TGCCGTGTGA ACCATGTGAC TTTGTCACAG CCAAGATNG      360
TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT                                400

```

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT      60
CCAGCTGCCC CGGCGGGGGA TGCGAGGCTC GGAGCACCCT TGCCC3GCTG TGATTGCTGC      120
CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA      180
GTTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA      240
AAAAAAA

```

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCCA CACAATGGCT ACCTTTAACA	60
TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTT ATAAATGCCT	180
GATTTAAAAA AAAAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 552 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTT AGGTTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCCT ATTCTTTATT	120
CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTGCCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTTCCCTG GCTAGAAAAA ATTATAACA GGACTTTGTT AGTTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTTTA	420
TTCCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TCGGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTCACG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTAAACT TTCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300

TCTTCTAAGT	CCTCTTCCAG	CCTCACTTTG	AGTCCTCCTT	GGGGGTTGAT	AGGAANTNTC	360
TCTTGGCTTT	CTCAATAAAA	TCTCTATCCA	TCTCATGTTT	AATTTGGTAC	GCNTAAAAAT	420
GCTGAAAAAA	TTAAATGTT	CTGGTTTCNC	TTTAAAAAAA	AAAAAAAAAA	AAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG	TATGCCNTCN	CTGTGGNGTT	ATTGTTGCTG	CCACCCTGGA	GGAGCCCAGT	60
TTCTTCTGTA	TCTTTCTTTT	CTGGGGGATC	TTCCTGGETC	TGCCCCCTCA	TTCCCAGCCT	120
CTCATCCCCA	TCTTGCACTT	TTGCTAGGGT	TGGAGGCGCT	TTCCTGGTAG	CCCCTCAGAG	180
ACTCAGTCAG	CGGAATAAG	TCCTAGGGGT	GGGGGGTGTG	GCAAGCCGGC	CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC	AGAAGCTAAA	GCCAAAGCCC	AAGAAGAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAGTA	CCAATAACAT	GCCAGTGCCA	GTGCCAGCAC	CAGTGGTGGC	TTCAGTGCTG	120
GTGCCAGCCT	GACCGCCACT	CTCACATTTG	GGCTCTTCGC	TGGCCTTGGT	GGAGCTGGTG	180
CCAGCACCAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	CAAGTGAGAT	TTTAGATATT	240
GTTAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGCTGCATC	CTCAGAAACC	TACTCAACAC	300
AGCACTCTNG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	CTCTGCATTA	AATCTATTTG	360
CCATTTCAAA	AAAAAAAAAA	AAA				383

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCCTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCGATTGAT	360
TATGCTTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTTT	420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCTC CTGGGGCCCA GGCGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTTCC TACACATTG GGCAAAGTAG AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA      240
GTGATTCTG CATGTCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNGGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNGC GCNTNCCTTT      480
T

```

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCATT      60
ACTTGGA AAA GCAACTTNA GCCTGGACAC TGGTATTAAA ATTCACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCATCACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTAC ACCTGT TAAA AGGGCGCTAA GCATTTTTGA TTCAACATCT TTTTTTTTGA      240
CACAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACCTTTCTT      300
CATGGGACAG AGCCATTTGA TTTAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG      472

```

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

AGAAACCACT ATCTCTNAAA ACAACCTCTC ATACCTTG TG GACCTAATTT TGTGTGCGTG      60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG      120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT      180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT      240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG      300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA      360

```

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTTT TTT 413

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 448 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCCTCCCC CGCGTCCCCG	60
GTCTAGCCN ACCATGGCCG GGCCCCCTGC CGCCCCGCTG CTCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CCGCGGCCG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCCTG GACTTTGCCG	240
TCGGCNANTA CAACAAACC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAGAA CCNAGCCAAT TNGAACAATT NCCCTCCAT AACAGCCCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATTTT	448

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA	60
GTAAGTATTC TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCCA GTGTTTTAGT CCTTGCATC	240
TTTATGTTN AGACTTGCCCT CTNTNAAATT GCTTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTTGA ATATCTTACA TCTNAAATN	360
AATTCTCTCC CCATANNAAC ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN	420
AATTCNNANA ANTTCAGNTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCGGAC	TGTTCANCCA	CCAACCTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGTCTGTAA	GCNTNTTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAG	TCACATCTTC	TAGGACCTTT	TTGGATTTCAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTTGTGA	AGACTTCATC	TGGTAAAGTC	TTAAGTTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTTAAATA	TACTTAATAG	GGCATTGGTN	CAC TAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCTCTTT	GACTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAA	CTGGCACTTG	NCTGGAAC TA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCACT	300
TGTCAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTGTT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTTCCT	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

ATACAGCCCA NATCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGCGGTCACT      60
GGTCCCCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGTTTGATGC TGCACCTCTT      120
CCCACGCAGG CAGCAGCGGG GCCGGTCAAT GAACTCCACT CGTGGCTTGG GGTGACGGT      180
TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCCGACT GTGCGGGACC      240
TGCAGCGAAA CTCCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCCAGG GCCTTGCCCA      300
GAACCTTCCG CCTGTTCTCT GCGGTCACCT GCAGCTGCTG CCGCTNACAC TCGGCCTCGG      360
ACCAGCGGAC AAACGGCGTT GAACAGCCGC ACCTCACGGA TGCCCANTGT GTCGCGCTCC      420
AGGAACGGCN CCAGCGTGTC CAGGTCAATG TCGGTGAANC CTCCGCGGGT AATGGCG      477

```

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

GAACGGCTGG ACCTTGCCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC      60
AGTCCGAGCA GCCCCAGACC GCTGCCGCCC GAAGCTAAGC CTGCCTCTGG CCTTCCCCTC      120
CGCCTCAATG CAGAACCANT AGTGGGAGCA CTGTGTTTAG AGTTAAGAGT GAACACTGTN      180
TGATTTTACT TGGGAATTTT CTCTGTTATA TAGCTTTTCC CAATGCTAAT TTCCAAACAA      240
CAACAACAAA ATAACATGTT TGCCTGTTNA GTTGATAAAA AGTANGTGAT TCTGTATNTA      300
AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTTATTGG TNCTCTGGAA      360
ATAAATATAT TATTAAA      377

```

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

CCCTTTGAGG GGTTAGGGTC CAGTTCCTCAG TGAAGAAAC AGGCCAGGAG AANTGCGTGC      60
CGAGCTGANG CAGATTTCCT ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT      120
CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG      180
GAAGGCCCCA TTCCGGGGCT GTTCCCGGAG GAGGAAGGGA AGGGGCTCTG TGTGCCCCC      240
ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCTT CACGTGTATC CCCACACAA      300

```

TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC	360
ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNNAAGG GGGCAGAATC TCCAATAGAN GGANNGAACC CTTGCTNANA	480
AAAAAAAAANA AAAAA	495

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTACTTG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
TAGCTGTTTT	GAGTTGATTC	GCACCACTGC	ACCACAACCTC	AATATGAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTGAAAA	GTATACAATG	AAAATTTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTTT	CACAGTAATA	TATGCCTTTT	GTAACCTCAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTTCTTT	CCTTGTTTAC	GTTAATTTTG	AAAAGAATGC	AT	472

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATTA	TATGTAACCT	CTACTAGTTT	TACTTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTTT	180
ATTCTTCACA	GATAGATGATG	AAAGAGTCCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAAT	300
TGTGTTAGTC	TCAATTCCTA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TAAATCTTCT	AGCTTT	476

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA 60  
 AAATAATGCT GCAAACCTTA TGTTCCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA 120  
 CAATCGCAAA TCAAACTCA CAAGTGCTCA TCTGTTGTAG ATTTAGTGA ATAAGACTTA 180  
 GATTGTGCTC CTTCGGATAT GATTGTTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT 240  
 CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT 300  
 GTGATTATNA AATTAATCAC AAATTTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT 360  
 NTNNTTTTNA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG 420  
 TTCNATCTTA TTTTTCCTN GACNACTANT TNCTTTTITA GGGNCTATTC TGANCCATC 479

(2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCTTGA TCAAGTTTGT GGCAGTACA ATCAGACCTA 60  
 TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA 120  
 TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA 180  
 AGTGATTCAG TTTCTCTTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA 240  
 TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACA GAGAAATAAA GTCAGAAAAAT 300  
 TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCAT TGAACCTTCT CTTAAGGACT 360  
 TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC 420  
 TTTGGAATAA TCTTGACGCT CCTGAACCTG CTCCTCTGCG A 461

(2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT 60
CGGCGCCTCT GCGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCCT 120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCGTGCC TTGGGGGTAC C 171

```

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGACGAA GATTCTGCCA GCAGTTGGTC 60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC 120
AAGGCTGAGC TGACGCCGCA GAGTCGTGT CACGTCCCAG GACCTTGACG CCGTCGGGGA 180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCCTCGGG AAGGGCGGCC 240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC 269

```

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA 60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTCTG GTCAACTTCC TTTGTCGTGG 120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG 180
AGTGGGTGCA CCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG 240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTTT AGAGAGTCCA 300
CTGTTCTGGA GGGAGATTAG GGTTCCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG 360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA 405

```

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT      60
GGCACTTAAT CCATTTTAT TCAAAATGT CTACAAATTT AATCCCATTA TACGGTATTT      120
TCAAAATCTA AATTATTCAA ATTAGCCAAA TCCTTACCAA ATAATACCCA AAAATCAAAA      180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAGGAA ATATATACGG CTGGTGTGTTT      240
CAAAGTACAA TTATCTTAAC ACTGCAAACA TTTTAAGGAA CTAAAATAAA AAAAAACACT      300
CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC      360
AAATCTTAGG GGAATATATA CTTACACGG GATCTTAAT TTTACTCACT TTGTTTATTT      420
TTTAAACCA TTGTTTGGGC CCAACACAAT GGAATCCCCC CTGGACTAGT                    470

```

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTTACT      60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC      120
TAAATGGAAA CTGCCCTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCCTAAAGT      180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTTGTAAAAC ATCCAAATTC      240
ATTTTCTCTG TCTTTAAAT TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATTT      300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTAATATTAG TAAGTGGCTT TTTTCCTAAA      360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTGAT ATTTCTACCT      420
ACGTTAATAA AATAGCATTT TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTTATGT      480
CCATTTTAGT CACTAAACGA TATCAAAGTG CCAGAATGCA AAAGGTTTGT GAACATTTAT      540
TCAAAAGCTA ATATAAGATA TTTACATAC TCATCTTTCT G                    581

```

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
TTTTTTTTTT TTTTTTTTTT TTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT 60
CACTCTCTAG ATAGGGCATG AAGAAACTC ATCTTCCAG CTTTAAAATA ACAATCAAAT 120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTCTCCTGA 180
AGGAAATCTG TTCATTCTTC TCATTATAT AGTTATATCA AGTACTACCT TGCATATTGA 240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT 300
TTCATGCAAA CTAGAAAATA ATGTTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT 360
CAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC 420
AAATCACATT TACGACAGCA ATAATAAAC TGAAGTACCA GTTAAATATC CAAAATAATT 480
AAAGGAACAT TTTTAGCCTG GGTATAATTA GCTAATTCAC TTTACAAGCA TTTATTAGAA 540
TGAATTCACA TGTTATTATT CCTAGCCCAA CACAATGG 578
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
TTTTTTTTTT TTTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATTT AAAATTCATA 60
GAAAAGTGCC TTACATTTAA TAAAAGTTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT 120
GTCTTGAACA CCAATATTAA TTTGAGGAAA ATACACCAA ATACATTAAG TAAATTATTT 180
AAGATCATAG AGCTTGTAAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTA 240
AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTTAATTTTG TGATGAATAT 300
GGGGTGTAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA 360
TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTTCT CTTTCTTCAA TCTTTTAAGG 420
GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTCTTTTCTA TGGAAGGATT 480
AGATATGTTT CCTTGCCAA TATTAAAAAA ATAATAATGT TTACTACTAG TGAAACCC 538
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT TTTTITAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTT 60  
ATTTATTAGC TCTGCAACTT ACATATTTAA ATTAAAGAAA CGTTTTAGAC AACTGTACAA 120  
TTTATAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCT CCAAGAGTGG ATGTGTCCCT 180  
TCTCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT 240  
GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG 300  
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAT 360  
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA 420  
CCGCTTCCTC AAAGGCGCTG CCACATTTGT GGCTCTTTCG ACTTGTTCAT AAA 473

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA CTGCAGGGCA TCTCGGTCAT GGAGCTGTCC GGCCTGGCCC CGGGCCCCTT 60  
CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGGACC GGCCCGGCTC 120  
CCGTACGAC GTGAGCCGCT TGGGCGGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA 180  
GCCGCGGGA GCCGCGTGC TGCGGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC 240  
CTTCCGCCGC GGTGTCATGG AGAACTCCA GGTGGGCCCA GAGATTCTGC AGCGGGAAAA 300  
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCCGGTT 360  
AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCCAGTGTT CTCTCAAAAA TTGGCAGAAG 420  
TGGTGAGAAT CCGTATGCCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT 480  
GTGTGCACTG GGCATTATAA TGGCTCTTTT TGACCGCACA CGCACTGACA AGGGTCAGGT 540  
CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTTCTGT GGAAAAGTCA 600  
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT 660  
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGGAGCAA TAGAACCCCA 720  
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACTTC CCAATCAGAT 780  
GAGCATGGAT GATTGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTTG CAAAGAAGAC 840  
GAAGGCAGAG TGGTGCAAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGTTTCTGAC 900  
TTTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCAGTGA 960  
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCAG CCATCCCTTC 1020  
TTCAAAAGG GATCCTTTCA TAGGAGAACA CACTGAGGAG ATACTTGAAG AATTTGGATT 1080  
CAGCCGCGAA GAGATTTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA 1140  
AGCTAGTCTC TAACTTCCAG GCCCAGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG 1200  
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTTA 1260  
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA 1320  
AATGGTTATC ATTAGGGCTT TTGATTTATA AAACCTTGGG TACTTATACT AAATTATGGT 1380  
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTC TTGACTTATA 1440  
TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATTT 1500  
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGTAT 1560

AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620  
A 1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro  
1 5 10 15  
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val  
20 25 30  
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg  
35 40 45  
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala  
50 55 60  
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe  
65 70 75 80  
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln  
85 90 95  
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln  
100 105 110  
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala  
115 120 125  
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr  
130 135 140  
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys  
145 150 155 160  
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys  
165 170 175  
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser  
180 185 190  
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg  
195 200 205  
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
210 215 220  
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
225 230 235 240  
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
245 250 255  
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
260 265 270  
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
275 280 285  
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TCPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGGACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCCTACT	GAGCCAGCGC	CTGCGCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCGACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGGCCG	CACTGTCTCT	TGCATCGACT	TCATGGTTTT	CACGGTGCGG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCC	AGATCGTCA	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCTCTGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGA	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATTC	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCAGTAT	GCCAACTGGC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCTCTG	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTGCGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGA	AGGCGCAGCG	TTACCGCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCGCGCTG	GCCCCGCCCT	TTATCGTCA	CTCCCACTTG	780
CGCCTCCTGC	TCAGGCAATT	GTGCAAGCGA	CCCGGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGCTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCGCGTC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCTTGC	TGCCCCCAGC	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGCACTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCCC	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCC	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCTCACA	CTGGGGAAAT	AAAGCCATTT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3410 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCCGA	TCCCAGGCCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACCTCEAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTGCGCAG	GCCTACTCTG	TCTATGCCTT	780
CATGATCAGT	CTTGGGGGCT	GCTTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCCTC	TTTGGCCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCCCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCCG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCCGC	ACCCTGCGCC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTTACA	CGGATTTCGT	GGGCGAGGGG	CTGTACCAGG	GCGTGCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGCAGCCT	1260
GGGGCTGTTT	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTG	GGCACTCGAG	CAGTCTATTT	GGCCAGTGTG	GCAGCTTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCCG	1440
GTTACCTTTC	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCCTGCCCA	AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCACCC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCAGTGCCT	ATATGGTGTG	1860
TGCCGCAGGC	CTGGGTCTGG	TCGCCATTTA	CTTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGGA	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCEGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTTG	TAGGGGAAGA	2460

GTCCTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC CACAGCACTG TCTTTTTTGCT 2520  
 GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTTGCCATCA 2580  
 CAGAGACACA GGCATTTAAA TATTTAACCT ATTTATTTAA CAAAGTAGAA GGAATCCAT 2640  
 TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA 2700  
 GGTCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT CTCCTGGGGT 2760  
 CTGGCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC TACTCATCCC AAATGATAAT 2820  
 TCCAAATGCT GTTACCCAAG GTTAGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT 2880  
 CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCTGGTTCCC CCCACTTCCA 2940  
 CTCCCCTCTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAAT TTCCCCTACC 3000  
 CCAACTTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCTGTT TGGAGCTACT 3060  
 GCAGGACCAG AAGCACAAG TCGGTTTCC CAAGCCTTG TCCATCTCAG CCCCAGAGT 3120  
 ATATCTGTGC TTGGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG 3180  
 GAGGTCTTAT CTCTCAGGGG GGGTTTAAGT GCCGTTTCCA ATAATGTCGT CTTATTTATT 3240  
 TAGCGGGGTG AATATTTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA 3300  
 AAATTAAAGG CTTTCTTATA TGTTTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360  
 AAAAAAARA AAAAAAAAAA AAAAAAAAAA AAAAAATAA AAAAAAAAAA 3410

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCCTTT 60  
 GTGGAGCCTC AGCAGTCCC TCTTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA 120  
 CCATGCAGTG CTTCACTTC ATTAAGACCA TGATGATCCT CTTCAATTTG CTCATCTTTC 180  
 TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTTC 240  
 TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCACGTG GGCTACTTCC 300  
 TCATCGCAGC CGGCGTTGTG GTCTTTGCTC TTGGTTTCCT GGGCTGCTAT GGTGCTAAGA 360  
 CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CTTCTCATC TTCATTGCTG 420  
 AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT 480  
 TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCCA GGAAGACTTC ACTCAAGTGT 540  
 GGAACACCAC CATGAAAGGG CTGAAGTGCT GTGGCTTCAC CAACTATACG GATTTTGAGG 600  
 ACTCACCTA CTTCAAAGAG AACAGTGCCT TTCCCCCATT CTGTTGCAAT GACAACGTCA 660  
 CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT 720  
 GCTTCAATCA GCTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG 780  
 CTGGAATTGG GGGCTCGAG CTGGETGCCA TGATTGTGTC CATGTATCTG TACTGCAATC 840  
 TACAATAAGT CCACTTCTGC CTCTGECAT ACTCTGCCA CATGGGAACT GTGAAGAGGC 900  
 ACCCTGGCAA GCAGCACTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA 960  
 GAATGGACCT GCCCTTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTTAGCG 1020  
 ATGCCTGACT TTCCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080  
 GTAGCCAGTT CTGTTGCCCA TTCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC 1140  
 TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200  
 AAGTGAAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC 1260  
 TGTTACAATG TTAATAAAAA AAAAAAAAAA 1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1           5           10           15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20           25           30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35           40           45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50           55           60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65           70           75           80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85           90           95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100           105           110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115           120           125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130           135           140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145           150           155           160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165           170           175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln
180           185           190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195           200           205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

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210 215 220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
1 5 10 15

Gln Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
 115 120 125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190  
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205  
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

50                      55                      60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65                      70                      75                      80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
                     85                      90                      95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
                     100                      105                      110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
                     115                      120                      125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
                     130                      135                      140  
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
                     145                      150                      155                      160  
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
                     165                      170                      175  
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
                     180                      185                      190  
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
                     195                      200                      205  
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
                     210                      215                      220  
 Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
                     225                      230                      235                      240  
 Gln

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:



GCTCTTTCTC	TCCCCTCCTC	TGAATTTAAT	TCTTTCAACT	TGCAATTTGC	AAGGATTACA	60
CATTTCACTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTTGT	TTAAAATTAC	120
TTGGTTTGTG	AATCCATCTT	GCTTTTTCCT	CATTGGAACT	AGTCATTAAC	CCATCTCTGA	180
ACTGGTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAACC	ATTTCAACCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
TTAGTC						366

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCTC	ATATTATAGC	AAAATTAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTTCATAT	TTTAAGACAC	ATGATTTATC	CTATTTTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCCT	TT		282

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTTATCCT	CCCTCCTGAA	ACAATTGCAA	AATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGCAA	AATATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCAGT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGGAA	ACAGATGAGG	TCACCTCTGT	240
GACTGCCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTTCAGAC	AGGGAGAAAT	300
TGGGT						305

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAATC TGAGTGGA   60
AANTCCTGGG T                                     71
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA   60
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC   120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT   180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT                               212
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC   60
CTCCGCCCGC GCAGAACATG CTGGGGTGGT                               90
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTTGA 60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG 120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCCTTTG GGAATTCCTT TACGATNGCC 180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA 218
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG 60
CATTGTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT 120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T 171
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA 60
TTATCAANTA TTGTGT 76
```

(2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT      60
CAATGTGCTG GGTCATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG      120
TTAAGATTTG T                                     131
```

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG      60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA      120
CTACAGTCTG CATTGTCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT      180
TTGCCTCACC AAACAAAAGT GAAACAACCTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG      240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC      300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTTGCA AGAATCTCAG      360
CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC      420
CTCTTTGCTT GT                                     432
```

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTTG AATAGTAAAA TAGAACTGA GCTGAAATTT CTAATTCACCT TTCTAACCAT 60  
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAANAATTT GT 112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG 54

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCCT CTACCAGCTC 60  
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA 120  
TTCTCTCTGA AGTCTAGGTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTC 180  
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTAGAATGG TTTTCCTTTT TCTTAGCCTT 240  
TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT 300  
AGGCTGCCTT CTTTCCATG TCC 323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC	60
TGAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTTCATC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA	60
TATAATGACG CAACAAAAG GTGCTGTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTTCCATTG TGTTTGGCG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTTTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAT CTGATGTGAT TTGGTTTATT ATCCAATAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

ACTTTTGCCA TTTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC      60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT      120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT      180
TTTAGCAAGT TAAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG      240
GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT      300
GTAACAATCT ACAATTGGTC CA                                     322

```

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

ACAAGCCTTC ACAAGTTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT      60
CTTGTTTTTC TTTCCATCTG GCTCCTGGGT TGACAATTG TGGAAACAAC TCTATTGCTA      120
CTATTTAAAA AAAATCACAA ATCTTTCCCT TTAAGCTATG TTNAATTCAA ACTATTTCCTG      180
CTATTCCTGT TTTGTCAAAG AAATTATATT TTTCAAAATA TGTNTATTTG TTGATGGGT      240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG                                     278

```

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAACA 60  
 TGATTCTCTG AGGTAAACT TGGTTTCAA ATGTTATTTT TACTTGTATT TTGCTTTTGG 120  
 T 121

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC ATGCCTAGCA CATCAGAATC CCTCAAAGAA CATCAGTATA ATCCTATACC 60  
 ATANCAAGTG GTGACTGGTT AAGCGTGCGA CAAAGGTCAG CTGGCACATT ACTTGTGTGC 120  
 AAAC TTGATA CTTTGTCTCT AAGTAGGAAC TAGTATACAG TNCCTAGGAN TGGTACTCCA 180  
 GGGTGCCCCC CAACCTCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACTTTCGCT 240  
 CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG 300  
 TTCCAAGGA TGCAAAGCCT GGTGCTCAAC TCCTGGGGCG TCAACTCAGT 350

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT 60  
 GCTGTGATTG TATCCGAATA NTCCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT 120  
 GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA 180  
 CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAACNCCAAG 240  
 AAAACTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC 300  
 TCCCAGGAAC CCGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG 360  
 GGTGCAGANG GATGAAGCAG CCAGNTGTTC TGCTGTGGT 399

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs



(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG	TNGGGGGTGA	TGCTGGTGGT	ANAAGTTGAN	GTGACTTCAN	GATGGTGTGT	60
GGAGGAAGTG	TGTGAACGTA	GGGATGTAGA	NGTTTTGGCC	GTGCTAAATG	AGCTTCGGGA	120
TTGGCTGGTC	CCACTGGTGG	TCACTGTCAT	TGGTGGGGTT	CCTGT		165

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA	ATGCCACATT	CACAACAGAA	TCAGAGGTCT	GTGAAAACAT	TAATGGCTCC	60
TTAACTTCTC	CAGTAAGAAT	CAGGGACTTG	AAATGGAAAC	GTTAACAGCC	ACATGCCCAA	120
TGCTGGGCAG	TCTCCCATGC	CTTCCACAGT	GAAAGGGCTT	GAGAAAAATC	ACATCCAATG	180
TCATGTGTTT	CCAGCCACAC	CAAAAGGTGC	TTGGGGTGGA	GGGCTGGGGG	CATANANGGT	240
CANGCCTCAG	GAAGCCTCAA	GTTCCATTCA	GCTTTGCCAC	TGTACATTCC	CCATNTTTAA	300
AAAAACTGAT	GCCTTTTTTT	TTTTTTTTTG	TAAATTC			338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG	GTTTTTGGCA	TCTGGTTTGC	CTATAGCCGA	GGCCACTTTG	ACAGAACAA	60
GAAAGGGACT	TCGAGTAAGA	AGGTGATTTA	CAGCCAGCCT	AGTGCCCGAA	GTGAAGGAGA	120
ATTCAAACAG	ACCTCGTCAT	TCCTGGTGTG	AGCCTGGTCG	GCTCACCGCC	TATCATCTGC	180

100

ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCGTGAT GTCTGTAGTT TCACAGGATG 240  
 CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT 300  
 GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCCTACCA CTGCTGAGTG 360  
 GCCTGGAAGT TGTTTAAAGT GT 382

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTTCTGTTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT 60  
 ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG 120  
 TTTTCACATT TCAACTTGTA TGTGTTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTT 180  
 ATATTCAGCA TAAAGGAGAA 200

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG 60  
 GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTT 120  
 ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA 180  
 AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG 240  
 TTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG 300  
 ATTCACAAAC CAAGTAATTT TAAACAAAGA CACTT 335

## (2) INFORMATION FOR SEQ ID NO:142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

ACCAGGTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGTATTTA      60
GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT      120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA      180
CACATGGTCC AACAACTCTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC      240
TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA      300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA      360
AGTACCAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT      420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT                               459

```

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTCTTAT CACCTGAGGG      60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG      120
ACCATCCGAC TTCCCTGTGT                               140

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTTT GTCATTTTCT      60
ATCTATACCA CTCTCCCTTC TGAAAACAA AATCACTANC CAATCACTTA TACAAATTTG      120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAG ATGT                               164

```

(2) INFORMATION FOR SEQ ID NO:145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

ACGTAGACCA TCCAAC TTG TATTTGTAAT GGCAACATC CAGNAGCAAT TCCTAAACAA      60
ACTGGAGGGT ATTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT      120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGTG ATAAACTTCA      180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG      240
TAGTAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT      300
CAA                                                                303

```

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC      60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GETCCTTTGC CAACAGGCCT      120
CCAAGTCAGG GCTGGGATTT GTTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT      180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGAACAAGC TGCCACTTTC TAAAGTAGCC      240
AGACTTGCCC CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG      300
TAGGGGTGAG CTGTGTGACT CTATGGT                                     327

```

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG 60  
 ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT 120  
 ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT 173

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACTT TATCTCATCG AATTTTAAAC CCAAACCTCAC TCACTGTGCC TTTCTATCCT 60  
 ATGGGATATA TTATTTGATG CTCCATTTC TACACATAT ATGAATAATA CACTCATACT 120  
 GCCCTACTAC CTGCTGCAAT AATCACAATC CTTTCCTGTC CTGACCCTGA AGCCATTGGG 180  
 GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC 240  
 NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA 300  
 TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG 360  
 CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT 420  
 CCAGGCACAG GCTACCTCAT CTTACAATC ACCCCTTTAA TTACCATGCT ATGGTG 477

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC 60  
 TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGSGGCCT 120  
 GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA 180  
 TTTCAAGCAG AGGGAACAGC AGTGAAA 207

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

104

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
ACCTTGATT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG      60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T      111
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC      60
AGCAAGATGG CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT      120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG      180
GTGCATCCGG CTCAGT      196
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC      60
CTTCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG      120
GAGGGAGTTT GT      132
```

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTATGGCC TCCAAACATG AAAGTGTGAG	60
CTTCTGCTCT TATGTCCTCA TCTGACAACT CTTTACCATT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGC GGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTTCAGCTC CCCTCCTCCG TGAACGAGA CTCTGATTTG	240
AGTTTCACAA ATTCTCGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG 60  
 GAAAGTGCTT TGGGAACCTGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT 120  
 TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC 180  
 ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT 240  
 GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG 300  
 GCCCTGGT 308

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA 60  
 TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACCTGA 120  
 GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT 180  
 CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT 240  
 AAAACCAGAT GTCTATCCTT AAGATTTTCA AATAGAAAAC AAATTAACAG ACTAT 295

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT 60  
 GAAGAGCAAA ACAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC 120  
 CTTAGT 126

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE: *Homo sapiens*
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

ACCCACTGGT CTTGGAAACA CCCATCCTTA-ATACGATGAT TTTTCTGTCG TGTGAAAATG 60
AANCCAGCAG GCTGCCCTTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT 120
GCCTGGGTAA TTCACCATT AATTCCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT 180
CTGGTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA 240
NATGTTTGTA GCCTTGCA TA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG 300
CCAACCCTGT TTTCCCAGTC CACGTAGACA GATTCACAGT GCGGAATTCT GGAAGCTGGA 360
NACAGACGGG CTCTTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG 420
TGTTTATTCT CTGATGTCCT GT 442

```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE: *Homo sapiens*

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAACTG ATGGGTGACG TTGTAGGTTT 60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG 120
GCTGCTGTGG ACTGTTGTTG ATTCCTCACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG 180
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC 240
TGCTGTGGTG CCGGGANGTG AANGTGTGTT GTCACCTGAG CTTGGCCAGC TCTGGAAGT 300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTAA 360
CGAACCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCTN 420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GCGNGCTGTG GAAGGTTGTA NATGTGTCACC 480
AAGGGAATAA GCTGTGGT 498

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

ACCTGCATCC AGCTTCCCTG CCAAACCTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC      60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT      120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC      180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCCC CATGACCCCA GATGCCTCTC      240
CCACCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTC TAACATCCTG      300
GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA      360
CTTGTAGAAT GAAGCCTGGA

```

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA      60
CACTGTCCAC TGGCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT      114

```

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTAA ATATCCTCAT ATATATCAAA      60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT      120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAACTAC TCACTGT      177

```

## (2) INFORMATION FOR SEQ ID NO:163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTATACAC GACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC 60  
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCGTGCACCTT 120  
CATCAGCGGC ATGATGT 137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGATGATCT TTGCCACCTT CGTGACTTTA 60  
TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA 120  
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACTGT 180  
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG 240  
GGTTATGACA AAGACAACCTG CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG 300  
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT 360  
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT 420  
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACTTT 469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG 60  
ATCCGCTGTC ATCCACTATT CTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC 120  
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT 180  
TCCTCTGAGA TGAGT 195

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC      60
CGAGGTCGGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT      120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT      180
TTTGACAGAC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG      240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC      300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT      360
NGGGGCCTTT TTGGTGAACT TTC                                     383

```

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT      60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC      120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC      180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC      240
TGANGTC                                     247

```

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATAATTCTCT AAAGGCTGTG GTAAGTTTGG CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCC CTACCACAAA AACAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAAGTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAGC TTCTGGGGGC CATCAGCTGC	420
TGGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTGA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGTAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA      60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCCTGG TGCATCCGCA GTGGGTGCTG      120
TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG      180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA      240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC      300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC      360
GCGGGGAACT CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC      420
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC      480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAGAA GGACTCCTGC      540
AACGGTGA CTGGGGGGCC CCTGATCTGC AACGGGTACT TGCAGGGCCT TGTCTCTTTC      600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC      660
ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCTATGAA      720
ATTGACCCCC AAATACATCC TGCGGAAGGA ATTCAGGAAT ATCTGTTCCC AGCCCCCTCT      780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC      840
CCCAGCCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC      900
CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC      960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC      1020
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA      1080
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTGGC ACGTTGACCC      1140
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTTCCTC TAGATCCAGA AATAAAGTTT      1200
AAGAGAAGNG CAAAAA AAAA AAAAAA AAAAAA AAAAAA      1248

```

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1           5           10           15

```

113

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
20 25 30

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
35 40 45

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
50 55 60

Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu  
65 70 75 80

Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe  
85 90 95

Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser  
100 105 110

Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe  
115 120 125

Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn  
130 135 140

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
145 150 155

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTACGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCCTGCT	CGCTAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCCTAC	CGCGGGAAC	TCTTGCTCTG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGTCTG	CCCTCTTCAA	GGAGGTCCTC	TGCCCACTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCCTGA	480
ACGTGTCTGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCAACCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCTGAT	CTGCAACGGG	TACTTGACAG	GCCTTGCTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720

AAACCGTCCA	GGCCAGTTAA	CTCTGGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGCGGA	AGGAATTCAG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCAGGAG	840
TCCAGGCCCC	CAGCCCCTCC	TCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCTCCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGGGTT	1020
GAGGCCCCCA	ACCCCTCCTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CCAGCCCCTC	TTCCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTTTCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTTCATTTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAA						1265

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs.
- (B) TYPE: nucleic acid.
- (C) STRANDEDNESS: single.
- (D) TOPOLOGY: linear.

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCTTGC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGCGGGGAA	CTCTTGCCCT	GTTTCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGTCT	GCCCTCTTCA	AGGAGGTCCT	CTGCCCAGTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAATGC	CTACCGTGCT	GCAGTGCGTG	AACGTGTCGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCGACT	540
CAGGGAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATTT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTTGTTGGA	ATTTTTTTGAT	ATTTCTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATTC	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGCC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAAAA	AAAAAAA					1459

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 1167 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTC TGCTC GGGCGTCTCTG      60
GTGCATCCGC AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCCTGC ACAGTCTTGA GGCCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCTTGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAACCTC TTGCCTCGTN TCTGGCTGGG GTCTGCTGGC GAACGGCAGA      360
ATGCCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCCAGCATG TTCTGCGCCG GCGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGGGGGGGCC CTGATCTGCA ACGGGTACTT GCAGGGCCTT      540
GTGTCTTTTCG GAAAAGCCCC GTGTGGCCAA CTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTC A CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCCTCCTC CCTCAGGCC AGGAGTCCAG GCCCCAGCC CCTCCTCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCTC CTCCTCAGA CCCAGGAGTC CAGACCCCC AGCCCCTCNT      840
CCNTCAGACC CAGGAGTCCA GCCCTCCTC CNTCAGACGC AGGAGTCCAG ACCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGTGCAAGC CCCCACCC TCNTCNTCA GAGTCAGAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC      1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TNCCTGTG CACAGTGECC CTTGTGGCA      1080
NGTTGACCCA ACCTTACCAG TTGGTTTTC ATTTTTTGTC CETTTCCCCT AGATCCAGAA      1140
ATAAGTNTA AGAGAAGCGC AAAAAAA 1167
  
```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1      5      10      15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20      25      30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
  
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCACTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAACTCTTGC	CTCGTTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCATCCA	GTCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTTCC	420
CAACCCTGGC	AGGGTTGTAC	CATTTCGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG 540  
 CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT 600  
 ACTAACCATG CCGATGTTTA GGTGAAATTA GCGTCACTTG GCCTCAACCA TCTTGGTATC 660  
 CAGTTATCCT CACTGAATTG AGATTTCTTG CTTCAAGGAT GCTGGTACTC CCCTCACAAA 720  
 TGACCTACAG AGGTGAGGGA TCATATAGCT CTTCAAGGAT GCTGGTACTC CCCTCACAAA 780  
 TTCATTTCTC CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCAGGG TGGGTGTGCA 840  
 GGTCACAATG ATGAATGTAT GATCGTGTTT CCATTACCCA AAGCCTTTAA ATCCCTCATG 900  
 CTCAGTACAC CAGGGCAGGT CTAGCATTTT TTCATTTAGT GTATGCTGTC CATTATGCA 960  
 ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTTGGG 1020  
 GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC 1080  
 TTAATAAACA GAAGCTGTGA TGTAAAAA AAAAAAAA 1119

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp  
 1 5 10 15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
 20 25 30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val  
 35 40 45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu  
 50 55 60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val  
 100 105 110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu  
 115 120 125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg  
 130 135 140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser

145 150 155 160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60
CCAGCTGCCC CCGGCCGGGG GATGCGAGGC TCGAGCACC CTGCCCCGGC TGTGATTGCT 120
GCCAGGCACT GTTCATCTCA GCTTTTCTGT CCCTTTGCTC CCGGCAAGCG CTTCTGCTGA 180
AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA 240
AAAAAAAAAA 250
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA 60
TCACCCAGAC CCCGCCCTG CCCGTGCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA 120
CTCTGCTACT CGGAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTT TATAAATGCC 180
TGATTTAAAA AAAAAAAAAA AA 202
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG 60
AATGTTTAGG CAGTGCTAGT AATTTCTCG TAATGATTCT GTTATTACTT TCCTNATTCT 120
TTATTCCTCT TTCTTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA 180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA 240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC 300
CTACTCTGTT CTTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTTT GGGAAGCCAA 360
ATTGATAATA TTCTATGTTT TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW 420
```

TTTTATTCCC AGGAATATGG KGTTTCATTTT ATGAATATTA CSCRGGATAG AWGTWTGAGT 480  
 AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTT 540  
 CAAAAAAAAA AAAAAAAAAA 558

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTGTTGA TCCAACCCIG GCTTWTTTTC 60  
 AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCMTG GCACCCCTGG 120  
 CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG 180  
 TTWGAATTC ACGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA 240  
 CTAAGGTAA ACTTTCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA 300  
 TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT 360  
 NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTAAATTGG TACGCATARA 420  
 AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC 60  
 AGTACCAGTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCAGTGCT 120  
 GGTGCCAGCC TGACCGCCAC TCTCACATTT GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT 180  
 GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTCCTCCT ACAAGTGAGA TTTTAGATAT 240  
 TGTTAATCCT GCCAGTCTTT CTCTTCAAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA 300  
 CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT 360  
 GCCATTTCAA AAAAAAAAAA AAAA 384

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYTNT CCRGTATKAC CTCAACGAGC 60

AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AACGCTTCAA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTTT	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTTG	CCAGCCATA	TCTTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTTCTCAT	ATTTTAAATT	ACTACMAGAW	TATTWMAGAW	WAAATGAWTT	GAAAAACTST	480
TAAAAA	AAAAA					496

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGACTTCC	60
CAAGTATCYT	GCGCSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTGGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGGCC	CAGGCGGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGCTGG	240
TGGTGCTGCT	CCTCGTCATC	TTCTGCTCG	TGGCCAAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTGGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360
GCGCAGCGTT	ACCGCCTCAT	CCGG				384

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CYTCTGGCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCAG	CTCTCTGACA	GTGAGGTCAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCCGAA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAAG	ACATTGACAA	ACTCGCCAG	420
GTGGAAAAAG	AMCAMCTCCT	GGARGTGCTN	GCCGCTCCTC	GTCMGTGGT	GGCAGCGCTW	480
TCCTTTTGAC	ACACAAACAA	GTAAAGGCA	TTTTTCAGCC	CCAGAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAAT			577

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid

121

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAAATYCATW	60
ACTKGGAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCACAAT	ATGCAACACT	120
TTAAACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTTCATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTC	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAGC	AAAAGTAAAC	AGTTATYAAT	TTGTTAGCCA	ATTCACCTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAATTGCA	TAAATATTGAG	CTTYGGGAGC	360
TGATATTTGA	GCGGAAGAGT	AGCCTTTCTA	CTTCACCAGA	CACAACTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTTA	CCACTTGCAC	AAGAAGGCGT	TTTCTTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTTT	TACTTTTGTG	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTAINT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAT	RMGTTWTKTT	WTTCTCCCTT	420
GCAAAAAACA	TGTACNGACT	TCCCGTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAACA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTTCAATG	TAAATGTTTG	CTAAAATACA	CTTTGAACTA	660
TTTTTCTGTN	TTCCCAGAGC	TGAGATNTTA	GATTTTATGT	AGTATNAAGT	GAAAAANTAC	720
GAAAATAATA	ACATTGAAGA	AAAAANANAAA	AAAAANAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180

AAGGCAGGGG CCACCAAGTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG 240  
 TGATAGGCAC AGGCCACCCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTCGACCAG 300  
 GTCATTGTGC CCTGCCCAGG CACAGCGTAN ATCTGGAAAA GACAGAATGC TTTCCTTTTC 360  
 AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTTNG GCTNGGTCTT GGTACNCTTG 420  
 GTTCGGCCCA GCTCCNCGTC CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCNGGNCCC 480  
 CC 482

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT TTTTAAACA GTTTTTCACA ACAAATTTA TTAGAAGAAT AGTGGTTTTG 60  
 AAAACTCTCG CATCCAGTGA GAACTACCAT ACACCACATT ACAGCTNGGA ATGTNCTCCA 120  
 AATGTCTGGT CAAATGATAC AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAAG 180  
 CGCTTTTGAC ATACAATGCA CAAAAAAAAA AGGGGGGGGG GACCACATGG ATTAAAATTT 240  
 TAAGTACTCA TCACATACAT TAAGACACAG TTCTAGTCCA GTCNAAAATC AGAACTGCNT 300  
 TGAAAAATTT CATGTATGCA ATCCAACCAA AGAACTTAT TGGTGATCAT GANTNCTCTA 360  
 CTACATCNAC CTTGATCATT GCCAGGAACN AAAAGTTNAA ANCACNCNGT ACAAAAAANAA 420  
 TCTGTAATTN ANTTCAACCT CCGTACNGAA AAATNTTNT TATACACTCC C 471

## (2) INFORMATION FOR SEQ ID NO:191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA AGGTCTGTTC TASTGTCGGM CTGTTACGCC ACCAACTCTA ACAAGTTGCT 60  
 GTCTTCCACT CACTGTCTGT AAGCTTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA 120  
 ATTCTTCACC AGTCACATCT TCTAGGACCT TTTTGGATTG AGTTAGTATA AGCTCTTCCA 180  
 CTTCTTTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTAGAAAGG AATTYAATTG 240  
 CTCGTTCTCT AACAATGTCC TCTCCTTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC 300  
 CTTTGTGCAT CCATTTTAAA TATACTTAAT AGGGCATTGK TNCAGTAGGT TAAATTCTGC 360  
 AAGAGTCATC TGTCTGCAAA AGTTGCGTTA GTATATCTGC CA 402

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC	120
ATGCTYTTT GAYTACCGTG TGCCAAGTGC TGGTGATTCT YAAACACACYT CCATCCCGYT	180
CTTTTGTTGA AAAACTGGCA CTTKTCTGGA ACTAGCARGA CATCACTTAC AAATTCACCC	240
ACGAGACACT TGAAAGGTGT AACAAAGCGA YTCTTGCAAT GCTTTTTGTC CCTCCGGCAC	300
CAGTTGTCAA TACTAACCCG CTGGTTTGCC TCCATCACAT TTGTGATCTG TAGCTCTGGA	360
TACATCTCCT GACAGTACTG AAGAACTTCT TCTTTTGTTC CAAAAGCARG TCTTGGTGCC	420
TGTTGGATCA GGTTCCTATT TCCAGTCYG AATGTTTACA TGGCATATTT WACTTCCAC	480
AAAACATTGC GATTTGAGGC TCAGCAACAG CAAATCCTGT TCCGGCATTG GCTGCAAGAG	540
CCTCGATGTA GCCGGCCAGC GCCAAGGCAG GCGCCGTGAG CCCACCAGC AGCAGAAGCA	600
G	601

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCC NATCCCACCA CGAAGATGCG CTGTGTTGACT GAGAACCTGA TGCGGTCACT	60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCYTT	120
CCCAACGCAG GCAGMAGCGG GSCCGGTCAA TGAATCCAY TCCTGGCTTG GGGTKGACGG	180
TKAAGTGCGA GAAGAGGCTG ACCACCTCGC GGTACCACAG GATGCCCGAC TGTGCGGGAC	240
CTGCAGCGAA ACTCCTCGAT GGTCATGAGC GGGGAAGCGAA TGAGGCCAG GGCCTTGCCC	300
AGAACCTTCC GCCTGTTCTC TGGCGTCACC TGCAGCTGCT GCCGCTGACA CTCGGCCTCG	360
GACCAGCGGA CAAACGGCRT TGAACAGCCG CACCTCACGG ATGCCAGTG TGTGCGCTC	420
CAGGAMMGC ACCAGCGTGT CCAGGTCAAT GTCGGTGAAG CCCTCCGCGG GTRATGGCGT	480
CTGCAGTGT TTTGTCGATG TTCTCCAGGC ACAGGCTGGC CAGCTGCGGT TCATCGAAGA	540
GTCGCGCCTG CGTGAGCAGC ATGAAGGCGT TGTCGGCTCG CAGTTCTTCT TCAGGAACCT	600
CACGCAAT	608

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG ACCTTGCTC GCATTGTGCT TGCTGGCAGG GAATACCTTG GCAAGCAGYT	60
CCAGTCCGAG CAGCCCCAGA CCGCTGCCGC CCGAAGCTAA GCCTGCCTCT GGCCTTCCCC	120
TCCGCCTCAA TGCAGAACCA GTAGTGGGAG CACTGTGTTT AGAGTTAAGA GTGAACACTG	180
TTTGATTTTA CTTGGGAATT TCCTCTGTTA TATAGCTTTT CCAATGCTA ATTTCCAAAC	240
AACAACAACA AAATAACATG TTTGCCTGTT AAGTTGTATA AAAGTAGGTG ATTCTGTATT	300
TAAAGAAAAT ATTACTGTTA CATATACTGC TTGCAATTTT TGTATTTATT GKTNCTSTGG	360
AAATAAATAT AGTTATTAAA GGTTGTCANT CC	392

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

CCSTTKGAGG GGTKAGGKYC CAGTTYCCGA GTGGAAGAAA CAGGCCAGGA GAAGTGCGTG      60
CCGAGCTGAG GCAGATGTTT CCACAGTGAC CCCCAGAGCC STGGGSTATATA GTYTCTGACC      120
CCTCNCAAGG AAAGACCACS TTCTGGGGAC ATGGGCTGGA GGGCAGGACC TAGAGGCACC      180
AAGGGAAGGC CCCATTCCGG GGSTGTTCCC CGAGGAGGAA GGGAAAGGGG TCTGTGTGCC      240
CCCCASGAGG AAGAGGCCCT GAGTCCTGGG ATCAGACACC CCTTCACGTG TATCCCCACA      300
CAAATGCAAG CTCACCAAGG TCCCCTCTCA GTCCCTTCC STACACCCTG AMCGGCCACT      360
GSCSCACACC CACCCAGAGC ACGCCACCCG CCATGGGGAR TGTGCTCAAG GARTCGCNGG      420
GCARCGTGGA CATCTNGTCC CAGAAGGGGG CAGAATCTCC AATAGANGGA CTGARCMSTT      480
GCTNANAAAA AAAAAANAAA AA                                     502

```

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC      60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT      120
WAGCTGTTTK GAGTTGATTS GCACCACTGC ACCCACAAC TCAATATGAA AACYAWTTGA      180
ACTWATTTAT TATCTTGTGA AAAGTATAAC AATGAAAATT TTGTTCATAC TGTATTKATC      240
AAGTATGATG AAAAGCAAWA GATATATATT CTTTTATTAT GTTAAATTAT GATTGCCATT      300
ATTAATCGGC AAAATGTGGA GTGTATGTTT TTTTCACAGT AATATATGCC TTTTGTAAC T      360
TCACTTGGTT ATTTTATTGT AAATGARTTA CAAAATCTT AATTTAAGAR AATGGTATGT      420
WATATTTATT TCATTAATTT CTTTCCTKGT TIACGTWAAT TTTGAAAAGA WTGCATGATT      480
TCTTGACAGA AATCGATCTT GATGCTGTGG AAGTAGTTTG ACCCACATCC CTATGAGTTT      540
TTCTTAGAAT GTATAAAGGT TGTAAGCCAT CNAACTTCAA AGAAAAAAT GACCACATAC      600
TTTGCAATCA GGCTGAAATG TGGCATGCTN TTCTAATTCC AACTTTATAA ACTAGCAAAN      660
AAGTG

```

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

TTTTNTTTTT TTTTTTTTGC AGGAAGGATT CCATTTATTG TGGATGCATT TTCACAATAT      60
ATGTTTATTG GAGCGATCCA TTATCAGTGA AAAGTATCAA GTGTTTATAA NATTTTTTAGG      120
AAGGCAGATT CACAGAACAT GCTNGTCNGC TTGCAGTTTT AECTCGTANA GATNACAGAG      180
AATTATAGTC NAACCAGTAA ACNAGGAATT TACTTTTCAA AAGATTAAAT CCAAAGTAA      240
CAAAATTCTA CCCTGAAACT TACTCCATCC AAATATTGGA ATAAAGTCA GCAGTGATAC      300
ATTCTCTTCT GAACTTTAGA TTTTCTAGAA AAATATGTAA TAGTGATCAG GAAGAGCTCT      360
TGTTCAAAAG TACAACNAAG CAATGTTCCC TTACCATAGG CCTTAATTCA AACTTTGATC      420
CATTTCACTC CCATCACGGG AGTCAATGCT ACCTGGGACA CTTGTATTTT GTTCATNCTG      480
ANCNTGGCTT AA

```

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

TTTNTTTTGN ATTTTCANTCT GTANNAANTA TTTTCATTAT GTTTATTANA AAAATATNAA      60
TGTTNTCCACN ACAAATCATN TTACNTNAGT AAGAGGCCAN CTACATTGTA CAACATACAC      120
TGAGTATATT TTGAAAAGGA CAAGTTTAAA GTANACNCAT ATTGCCGANC ATANCACATT      180
TATACATGGC TTGATTGATA TTTAGCACAG CANAAACTGA GTGAGTTACC AGAAANAAAT      240
NATATATGTC AATCNGATTT AAGATACAAA ACAGATCCTA TGGTACATAN CATCNTGTAG      300
GAGTTGTGGC TTTATGTTTA CTGAAAGTCA ATGCAGTTCC TGTACAAAGA GATGGCCGTA      360
AGCATTCTAG TACCTCTACT CCATGGTTAA GAATCGTACA CTTATGTTTA CATATGTNCA      420
GGGTAAGAAT TGTGTTAAGT NAANTTATGG AGAGGTCCAN GAGAAAAATT TGATNCAA      478

```

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCAGTGACA ATCAGACCTA      60
TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA      120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA      180
AGTGATTGAG TTTCTCTTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA      240
TGAAGCCNAC TCTGAACACG CTGGTTATCT NAGATGAGAA NCAGAGAAAT AAAGTCNAGA      300
AAATTTACCT GGANGAAAAG AGGCTTTNGG CTGGGGACCA TCCCATTGAA CCTTCTCTTA      360
ANGGACTTTA AGAANAAACT ACCACATGTN TGTTNGTATCC TGGTGCCNGG CCGTTTANTG      420
AACNTNGACN NCACCCTTNT GGAATANANT CTTGACNGCN TCCTGAACTT GCTCCTCTGC      480
GA

```

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGACGAA GATTCTGCCA GCAGTTGGTC      60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC      120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCAC GACCTTGACG CCGTCGGGGA      180
CAGCCGGAAC AGAGCCCGGT GAANGCGGA GGCCTCGGGG AGCCCTCGG GAAGGGCGGC      240
CCGAGAGATA CGCAGGTGCA GGTGGCCGCC

```

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA      60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTCC GTCAACTTCC TTTGTCGTGG      120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAANCGAAGC ANAANTAACA      180
TGGAGTGGGT GCACCCTCCC TGTAGAACCT GGTTACNAA GCTTGGGGCA GTTCACCTGG      240
TCTGTGACCG TCATTTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG      300
TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAA ATCCACNTGA      360
AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA      419

```

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT      60
TGGCACTTAA TCCATTTTAA TTTCAAAATG TCTACAAANT TTNAATNCNC CATTATACNG      120
GTNATTTTNC AAAATCTAAA NNTTATTCAA ATNTNAGCCA AANTCCTTAC NCAATNNAA      180
TACNCNCAA AATCAAAAAT ATACNTNTCT TTCAGCAAAC TTNGTTACAT AAATTAATAA      240
AATATATACG GCTGGTGTTC TCAAAGTACA ATTATCTTAA CACTGCAAAC ATNTTTNNAA      300
GGAACATAAA TAAAAAATAA CACTNCCGCA AAGGTTAAAG GGAACAACAA ATTCTNTTTA      360
CAACANCNNC NATTTATAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTACACNG      420
GGATCTTAAC TTTTACTNCA CTTTGTATTAT TTTTTTANAA CCATTGTNTT GGGCCCAACA      480
CAATGGNAAT NCCNCCNCNC TGGACTAGT

```

## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTTACT 60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC 120
TAAATGGAAA CTGCCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCCTAAAGT 180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTTGTAAAAC ATCCAAATTC 240
ATTTTCTCTG TCTTTAAAT TATCTAATCT TCCATTTTT TCCCTATTCC AAGTCAATTT 300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCTAAA 360
AGGGAAAACA GGAAGAGANA ATGGCACACA AAACAAACAT TTTATATTCA TATTTCTACC 420
TACGTTAATA AAATAGCATT TTGTGAAGCC AGCTCAAAAG AAGGCTTAGA TCCTTTTATG 480
TCCATTTTAG TCACTAAACG ATATCNAAG TGCCAGAATG CAAAAGGTTT GTGAACATTT 540
ATTCAAAAGC TAATATAAGA TATTTACAT ACTCATCTTT CTG 583

```

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

TTTTTTTTNT TTTTTTTTTT TTTTNTCTC TTCTTTTTTT TTGANAATGA GGATCGAGTT 60
TTTCACTCTC TAGATAGGGC ATGAAGAAAA CTCATCTTTC CAGCTTTAAA ATAACAATCA 120
AATCTCTTAT GCTATATCAT ATTTTAAGTT AAACATATGA GTCCTGGCT TATCTTCTCC 180
TGAAGGAAAT CTGTTTCATT TTCTCATTCA TATAGTTATA TCAAGTACTA CCTTGCATAT 240
TGAGAGGTTT TTCTTCTCTA TTTACACATA TATTTCCATG TGAATTTGTA TCAAACCTTT 300
ATTTTCATGC AAACATAGAAA ATAATGINTT CTTTTCGATA AGAGAAGAGA ACAATATNAG 360
CATTACAAAA CTGCTCAAAT TGTTTGTTAA GNTTATCCAT TATAATTAGT TNGGCAGGAG 420
CTAATACAAA TCACATTTAC NGACNAGCAA TAATAAAACT GAAGTACCAG TTAAATATCC 480
AAAATAATTA AAGGAACATT TTAGCCTGG GTATAATTAG CTAATTCAT TTACAAGCAT 540
TTATTNAGAA TGAATTCACA TGTTATTATT CCNTAGCCCA ACACAATGG 589

```

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```

TTTTNTTTTT TTTTTCAGT AATAATCAGA ACAATATTTA TTTTATATT TAAAATTCAT 60
AGAAAAGTGC CTTACATTTA ATAAAAGTTT GTTCTCAAAA GTGATCAGAG GAATTAGATA 120
TNGTCTTGAA CACCAATATT AATTGAGGA AAATACACCA AAATACATTA AGTAAATTAT 180
TTAAGATCAT AGAGCTTGTA AGTGAAAAGA TAAAATTTGA CCTCAGAAAC TCTGAGCATT 240
AAAAATCCAC TATTAGCAAA TAAATTAATA TGGACTTCTT GCTTTAATTT TGTGATGAAT 300
ATGGGGTGTC ACTGGTAAAC CAACACATTC TGAAGGATAC ATTACTTAGT GATAGATTCT 360
TATGTACTTT GCTANATNAC GTGGATATGA GTTGACAAGT TTCTCTTTCT TCAATCTTTT 420
AAGGGGCGNGA NGAAATGAGG AAGAAAAGAA AAGGATTACG CATACTGTTC TTTCTATNGG 480
AAGGATTAGA TATGTTTCCT TTGCCAATAT TAAAAAATA ATAATGTTTA CTACTAGTGA 540
AACCC

```

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```

TTTTTTTTTT TTTTITAGTC AAGTTTCTNA TTTTATTAT AATTAAAGTC TTGGTCATT 60
CATTATTAG CTCTGCAACT TACATATTTA AATTAAAGAA ACGTTNTTAG ACAACTGTNA 120
CAATTTATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT 180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTTA ATTTTATTAG TAGATNATAC 240
ACTGCTGCAA ACGCTAATTC TCTTCTCCAT CCCCATGTNG ATATTGTGTA TATGTGTGAG 300
TTGGTNAGAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT 360
TCGGTGAAAA TAGACTGTGT CTGTCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG 420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATTT GTGGCNTCTN TTGCACTTGT 480
TTCAAAA

```

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```

TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAA 60
TACATAGCAT TAAATCCCAA ATCCTATTTA AAGACCTGAC AGCTTGAGAA GGTCACACT 120
GCATTTATAG GACCTTCTGG TGGTCTGCT GTTACNTTGG AANTCTGACA ATCCTTGANA 180
ATCTTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTTTCA CAGAGGAANA ACACAGCGCA 240
GAAATGAAGG GGCCAGGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG 300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA

```

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

129

- (A) LENGTH: 524 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

AGGGCGTGGT GCGGAGGGCG TTAAGTTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG 60
GTTGTGTTCC GGCCCATCC AACCACGAAG TTGATTTCTC TTGTGTGCAG AGTGACTGAT 120
TTTAAAGGAC ATGGAGCTTG TCACAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC 180
TCCCGCGTGA TTCACATTTA GCAACCAACA ATAGCTCATG AGTCCATACT TGTAATAACT 240
TTTGGCAGAA TACTTNTTGA AACTTGCAGA TGATAACTAA GATCCAAGAT ATTTCCCAAA 300
GTAAATAGAA GTGGGTCATA ATATTAATTA CCTGTTTACA TCAGCTTCCA TTTACAAGTC 360
ATGAGCCCAG AACTGACAT CAACTAAGC CCCTTAGAC TCCTCACCAC CAGTCTGTCC 420
TGTCATCAGA CAGGAGGCTG TCACCTTGAC CAAATTCTCA CCAGTCAATC ATCTATCCAA 480
AAACCATTAC CTGATCCACT TCCGGTAATG CACCACCTTG GTGA 524
  
```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTG TTGCTCCTTG 60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA 120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA 159
  
```

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC 60
ACTGAATTTT TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA 120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT 180
TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA 240
CCAGGATGCT AAATCA 256
  
```

(2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG      60
ACTGGAACAC ATACCCACAT CTTTGTTCCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT      120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA      180
GGGGAGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA      240
AAAAAAGGAG CAAATGAGAA GCCT              264

```

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA      60
GGATTTAATG TTGTCTCAGC TTGGGCACCT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG      120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCCGCCAG      180
TTNAATTTCA TTCCCATTTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTTA      240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA      300
TTTTTTTTTC CTTTATTCCT TTGTCAGA              328

```

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAAGTGAATT CTCTCCAGTT      60
TAAAGCATTG CTAAGTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT      120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT      180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT      240
TCTCATCGGT              250

```

## (2) INFORMATION FOR SEQ ID NO:214:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

ACCCAGAATC CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTTG ATTGTCAAAG      60
GATTTAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG      120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT      180
TGAATTTTCA TCCCATTGAC TTGGGATCCT TATCATGAGC CANAGAGATT GAAAATTTAC      240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT      300
TTTTTTTTTC TTTATTCCTT TGTCAGAGAT GCGATTCATC CATATGCTAN AAACCAACAG      360
AGTGACTTTT ACAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT      420
ACTTTGCTCT CCCTAATATA CCTC                                     444
  
```

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AACTGAATT CTCTCCAGTT      60
TAAAGCATTG CTCCTGAAGG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT      120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT      180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT      240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA      300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCA GGTGGAAATC TCCTATACTT      360
GGTGCC                                     366
  
```

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC      60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTTNC ATTTTTTTAT      120
TAATAAAAAG TNNAAGGC CTCTTCTCAA CTTTTTTCCC TTNGGCTGGA AAATTTAAAA      180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT      240
  
```

AATTCTTCCT TCCCTCCTTT

260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCCTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCCTA	240
ATATCCTTCA TGCTTGTAAG GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTTG TAGTAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTTAC ATTTCTTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCTT TCATCTTGGA TTCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTGT CATAATCCAA	180
TTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATECC GGAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTGTAGGT TGCTTTTACA TATATCTGGC ATATTTGAGT	300
CTCGTATCAA AACAATAGAT TGGTAAAGGT GGTATTATTG TATTCATAAG T	351

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAGAAAA ATTATCTTAG	GGACTGATAT	60
TGGTAATTAT GGTCAATTTA ATWRTRTTKT GGGGCATTTT CTTACATTGT	CTTGACAAGA	120
TTAAAATGTC TGTGCCAAAA TTTTGTATTT TATTTGGAGA CTTCTTATCA	AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG	TGTGCTATTC	240
TAAAAGATTT TGATTTCTTG GAATGACAAT TATATTTTAA CTTTGGTGGG	GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGTC	ACTTGTTTGT	360
ACCATTAAGC TATATGTTTA AAA		383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC	AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA	AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA	AGAGAAGGAA	180
GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC	TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA	CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC		320

## CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
  - (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
  - (b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.
2. The method of claim 1 wherein the binding agent is a monoclonal antibody.
3. The method of claim 2 wherein the binding agent is a polyclonal antibody.
4. A method for monitoring the progression of prostate cancer in a patient, comprising:
  - (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
  - (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
  - (c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.
10. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies of claim 5; and
  - (b) a detection reagent.
11. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
  - (b) a detection reagent.
12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.
13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.
14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.
15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.
16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate



protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

—

100

— •

a301248\_0001.Dna /rev  
mest\_Rod12:Mmaa36804

D MMAA36804 standard; RNA; EST; 627 BP.  
C AA536804;  
V AA536804.1  
T 31-JUL-1997 (Rel. 52, Created)  
T 03-MAR-2000 (Rel. 62, Last updated, Version 2)  
E vj88f09.r1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:94420

E 3', mRNA sequence.

W EST.

S Mus musculus (house mouse)

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia

C Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

N [1]

P 1-627

A Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,  
A Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,  
A Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B.,  
A Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;  
RT "The WashU-HHMI Mouse EST Project";  
RL Unpublished.

DR RZPD; IMAGp998C182349; IMAGp998C182349.

DR RZPD; IMAGp998C182349Q0; IMAGp998C182349Q0.

CC On Sep 12, 1996 this sequence version replaced gi:1292316.

CC Contact: Marra M/Mouse EST Project

CC WashU-HHMI Mouse EST Project

CC Washington University School of MedicineP

CC 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

CC Tel: 314 286 1800

CC Fax: 314 286 1810

CC Email: mouseest@watson.wustl.edu

CC This clone is available royalty-free through LLNL ; contact the  
CC IMAGE Consortium (info@image.llnl.gov) for further information.  
CC MGI:541057

CC Possible reversed clone: polyT not found

CC High quality sequence stop: 469.

FH Key Location/Qualifiers

FH  
FT source

1. .627

FT /db\_xref="taxon:10090"

FT /db\_xref="ESTLIB:862"

FT /db\_xref="RZPD:IMAGp998C182349"

FT /db\_xref="RZPD:IMAGp998C182349Q0"

FT /note="Organ: embryo; Vector: pBluescribe (modified);

FT Site\_1: MluI; Site\_2: SalI; Cloned unidirectionally from  
FT mRNA prepared from 13,500 2-cell stage embryos. Primer:

FT SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. cDNAs

FT were cloned into the MluI/SalI sites of a modified  
FT pBluescribe vector using commercial linkers (NEB). Avera

FT insert size: 1.2 kb."

FT /organism="Mus musculus"

FT /strain="B6D2 F1/J" . . .

LORES Init1: 581 Initn: 581 Opt: 661 z-score: 767.4 E():  
70.9% identity in 278 bp overlap

0

a301248\_000 329 319 309 299 289 279  
GGCCCTCTAGACTCGAGCGGCCGCGTCGNCCAGGAGGATATTTACCCTCAGGAAATAGAT  
naa36804 GCTAAGGATGTATGTTTACCAGCTGCTATTTCAGCAGGATCCTCACCTCGGGAAACTGAT  
150 160 170 180 190 200

a301248\_000 269 259 249 239 229 219  
GCATCCAGCAACTATACTCCCCAAGATCCTGCAAGAAATGAAATCCACAGTGATAAGGCA  
maa36804 ATGTTTCAGTAAATCAGACCACAGTCTTCCTGCAATAAATGAGATTAATGATGAAAGTGAA  
210 220 230 240 250 260

a301248\_000 209 199 189 179 169 159  
CCTGTCTTATACCTACATGACCAGCTGTCAGAACTTCTAAAAGAGTTTCCTTATGGCATT  
maa36804 CCTATCTCATACTACATGACCAGCTGTCAGAGCTTTTAAAAGAGTTCCCTTATGGCATT  
270 280 290 300 310 320

sa301248\_000 149 139 129 119 109 99  
GAGGCTGTGAATACACGTGAAGGTTCTGTGGGCCAGCAAACTACATACCAGACCTCAGAA  
vmaa36804 GAAACTTTTAACAGACATGAAGTGTCTTTGGACCAACAAAAGACATAAAATCGTAGAA  
330 340 350 360 370 380

sa301248\_000 89 79 69 59 49 39  
GATCAAACTGCTGATAAAACCAGTTCTGACTCCAAAGACCCAGCAGATCAAATACAAATT  
mmaa36804 AATCAAACTGGTGGTAAACTAGTAATGTGTCTGGGGATAGCACAGACCAAATAAAATT  
390 400 410 420 430 440

sa301248\_000 29 19 9  
ACAATATTTCTTTCATTACTAGTGAGGTTG  
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450 460 470 480 490 500

a301248\_0001.Dna  
mhtg4:Ac016957

D AC016957 standard; DNA; HTG; 195002 BP.  
C AC016957;  
V AC016957.8  
T 14-DEC-1999 (Rel. 62, Created)  
T 02-JUN-2000 (Rel. 63, Last updated, Version 10)  
E Homo sapiens clone RP11-50I19, WORKING DRAFT SEQUENCE, 47 unordered pieces  
W HTG; HTGS\_DRAFT; HTGS\_PHASE1.  
S Homo sapiens (human)  
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
C Eutheria; Primates; Catarrhini; Hominidae; Homo.  
N [1]  
P 1-195002  
A Muzny D.M., Adams C., Bailey M., Barbaria J., Blankenburg K., Bodota B.,  
A Bouck J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J.,  
A Carter M., Chacko J., Chen Z., Cox C., David R., Delgado O., Deshazo D.,  
A Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,  
A Ferraguto D., Forcum-Tansey J., Frantz P., Ganesh R., Gorrell J.H.,  
A Gorrell L.L., Guevara W., Harris K., Hernandez J., Hodgson A., Hogues M.,  
A Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,  
A Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,  
A Liu J., Liu W., Logan O., Lozado R.J., Lu J., Lucier R., Martin R.,  
A Martinez C., McLeod M.P., Mei G., Morgan M., Morris S., Nash S., Nelson A  
A Nguyen R., Nguyen N., Nguyen S., Oswal G., Parish B., Paxton S., Payton B  
A Perez L., Pu L.L., Quiles M., Reiter D., Rives M., Samuel S., Say J.,  
A Scherer S., Shah E., Shen H., Simon M., Sparks A., Stamps A., Sugang R.,  
A Tabor P., Taylor T., Vasquez L., Vinson R., Vo Q., Wahbah M.,  
A Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,  
A Wren J., Wrensford G., Yu W., Zhou X., Nelson D., Gibbs R.;  
RT "Direct Submission";  
RL Unpublished.  
RN [2]  
RP 1-195002  
RA Worley K.C.;  
RT ;  
RL Submitted (09-DEC-1999) to the EMBL/GenBank/DBJ databases.  
RL Human Genome Sequencing Center, Department of Molecular and Human Genetic  
RL Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
CC On May 30, 2000 this sequence version replaced gi:8025078.  
CC -- Genome Center  
CC Center: Baylor College of Medicine  
CC Center code: BCM  
CC Web site: <http://www.hgsc.bcm.tmc.edu/>  
CC Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
CC -- Project Information  
CC Center project name: HMUV  
CC Center clone name: RP11-50I19  
CC -- Summary Statistics  
CC Sequencing vector: M13; L08821  
CC Chemistry: Dye-primer Bodipy: 9% of reads  
CC Chemistry: Dye-terminator Big Dye: 91% of reads . . .

CORES Init1: 1390 Initn: 1390 Opt: 1390 z-score: 1821.2 E():

0

100.0% identity in 278 bp overlap

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                  CAACCTCACTAGTAAATGAAAGAAATATTGTAATTTGTATTTGATCTGCTGGG
c016957          GGAAATATTTCTTTTCATTGCTCTGAGCTTAATATTGTAATTTGTATTTGATCTGCTGGG
                  27060      27070      27080      27090      27100      27110

a301248_000      60      70      80      90      100      110
                  TCTTTGGAGTCAGAACTGGTTTTATCAGCAGTTTGATCTTCTGAGGTCTGGTATGTAGTT
c016957          TCTTTGGAGTCAGAACTGGTTTTATCAGCAGTTTGATCTTCTGAGGTCTGGTATGTAGTT
                  27120      27130      27140      27150      27160      27170

a301248_000      120      130      140      150      160      170
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c016957          TGCTGGCCCCACAGAACCTTCACGTGTATTACAGCCTCAATGCCATAAGGAAACTCTTTT
                  27180      27190      27200      27210      27220      27230

a301248_000      180      190      200      210      220      230
                  AGAAGTTCTGACAGCTGGTCATGTAGGTATAAGACAGGTGCCTTATCACTGTGGATTTC
c016957          AGAAGTTCTGACAGCTGGTCATGTAGGTATAAGACAGGTGCCTTATCACTGTGGATTTC
                  27240      27250      27260      27270      27280      27290

a301248_000      240      250      260      270      280      290
                  TTTCTTGCAGGATCTTGGGGAGTATAGTTGCTGGATGCATCTATTTCTGAGGGTAAATA
c016957          TTTCTTGCAGGATCTTGGGGAGTATAGTTGCTGGATGCATCTATTTCTGAGGGTAAATA
                  27300      27310      27320      27330      27340      27350

a301248_000      300      310      320      330      340      350
                  TCCTCCTGGNCGACGCGGCCGCTCGAGTCTAGAGGGCCGTTTAAACCCGCTGATCAGCC
c016957          TCCTCCTGAATAGCAGCTGACGAGCACGTATCGTTAGCTGTGCTTTTTTCAGTGGCATGC
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a301248\_0001.Dna  
msyn:Af060226

D AF060226 standard; circular DNA; SYN; 5771 BP.  
C AF060226;  
V AF060226.1  
T 06-MAY-1998 (Rel. 55, Created)  
T 16-AUG-2000 (Rel. 64, Last updated, Version 2)  
E Eukaryotic expression vector pCR3.1mBCL-XL, complete sequence.  
W  
S Eukaryotic expression vector pCR3.1mBCL-XL  
C artificial sequence; vectors.  
N [1]  
P 1-5771  
A Pirtskhalaishvili G., Shurin G.V., Gambotto A., Esche C., Wahl M.,  
A Yurkovetsky Z.R., Robbins P.D., Shurin M.R.;  
T "Transduction of dendritic cells with Bcl-xl increases their resistance to  
T prostate";  
L J. Immunol. 165(4):1956-1964(2000).  
N [2]  
P 1-5771  
A Gambotto A., Pagliano O., Shurin M., Robbins P.D.;  
T ;  
L Submitted (17-APR-1998) to the EMBL/GenBank/DDBJ databases.  
L Vector Core Facility, University of Pittsburgh, 300 Technology Drive,  
L Pittsburgh, PA 15219, USA  
FH Key Location/Qualifiers  
FH  
FT source 1. .5771  
FT /db\_xref="taxon:75965"  
FT /organism="Eukaryotic expression vector pCR3.1mBCL-XL"  
FT promoter 1. .596  
FT /note="CMV"  
FT promoter 638. .657  
FT /note="T7; priming site also"  
FT CDS 747. .1448  
FT  
FT /codon\_start=1  
FT /note="BALB/c form"  
FT /product="murine BCL-XL"  
FT /protein\_id="AAC15799.1"  
FT /translation="MSQSNRELVVDFLSYKLSQKGYWSQFSDVEENRTEAPEETEA  
FT ETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR  
FT FSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQV  
FT SRIASWMATYLNHDHLEPWIQENGWDTFVDLYGNNAAESRKGQERFNRWFLTGMTV  
FT  
FT VLLGSLFSRK"  
FT misc\_feature 1524. .1541  
FT /note="pCR3.1 reverse priming site"  
FT rep\_origin 1827. .2500  
FT  
FT /note="ColE1"  
FT CDS complement(3082. .3870)  
FT /codon\_start=1  
FT /product="neomycin/kanamycin resistance protein"  
FT /protein\_id="AAC15800.1" . . .

CORES Initl: 427 Initn: 457 Opt: 427 z-score: 591.6 E(): 5.9e-25  
96.6% identity in 89 bp overlap

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TTCCTGAGGGTAAATATCCTCCTGGNCGACGCGGCCGCTCGAGTCTAGAGGGCCCGTTTA  
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f060226 AGCCGAATTCTGCAGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTA

1450 1460 1470 1480 1490 1500

a301248\_000 340 350 360 370 380 390  
AACCCGCTGATCAGCCTCGACTGTGCCTTCTANTTGCCANCCATNTGTTGTTTGCCCTC  
|||||

f060226 AACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC

1510 1520 1530 1540 1550 1560

f060226 CCCCCTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCTTTTCCTAATAAAATGA

1570 1580 1590 1600 1610 1620



301248\_0001.Dna  
mpatent:Ax001326

D AX001326 standard; DNA; UNC; 7108 BP.  
C AX001326;  
V AX001326.1  
T 10-MAR-2000 (Rel. 63, Created)  
T 10-MAR-2000 (Rel. 63, Last updated, Version 1)  
E Sequence 38 from Patent EP0892047.  
  
W  
S unidentified  
C unclassified.  
N [1]  
P 1-7108  
A Fleckenstein B.P., Ensser A.D.;  
T "Human and murine semaphorin L";  
L Patent number EP0892047-A/38, 20-JAN-1999.  
L HOECHST MARION ROUSSEL DE GMBH (DE).  
PH Key Location/Qualifiers  
PH  
FT source 1. .7108  
FT /db\_xref="taxon:32644"  
FT /organism="unidentified"  
FT exon 1. .7108  
SQ Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T; 0 other;

SCORES Init1: 427 Initn: 457 Opt: 427 z-score: 590.7 E(): 5.4e-25  
96.6% identity in 89 bp overlap

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Ax001326	TCATCATCATTGAGTTTATCCAGCACAGTGGCGGCGCTCGAGTCTAGAGGGCCCGTTTA					
	2620	2630	2640	2650	2660	2670
	340	350	360	370	380	390
Sa301248_000	AACCCGCTGATCAGCCTCGACTGTGCCTTCTANTTGCCANCCATNTGTTGTTTGCCCCT					
Ax001326	AACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTC					
	2680	2690	2700	2710	2720	2730
Ax001326	CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCCTGTCCTTTCCTAATAAAATGA					
	2740	2750	2760	2770	2780	2790



D X02662 standard; DNA; 7108 BP.  
C X02662;  
T 07-MAY-1999 (first entry)  
E EP-892047 Seq ID 38.  
W Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;  
W organ transplantation; inflammation therapy; immunotherapy; agonist;  
W immunomodulatory; antagonist; ss.  
S Homo sapiens.  
N EP892047-A2.  
D 20-JAN-1999.  
F 06-JUL-1998; 98EP-0112470.  
R 11-FEB-1998; 98DE-1005371.  
R 09-JUL-1997; 97DE-1029211.

SA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
SI Ensser A, Fleckenstein B;  
OR WPI; 1999-083564/08.  
PT New semaphorin L proteins - used as immunosuppressants and  
PT antiinflammatory agents in organ transplants, inflammation therapy,  
PT immunotherapy and gene therapy  
PS Disclosure; Page 96-100; 135pp; German.  
IC This invention describes a novel human semaphorin L protein. This protein  
IC or its encoding DNA are useful as immunosuppressants and/or  
IC anti-inflammatory agents in organ transplantation, inflammation therapy,  
IC immunotherapy and gene therapy. The DNA can be used to produce knock-out  
IC or knock-in animals for research purposes. The proteins or DNA can be  
IC used to search for the corresponding receptors or to screen for  
IC immunomodulatory agonists or antagonists.  
SQ Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T; 0 other;

SCORES Init1: 427 Initn: 457 Opt: 427 z-score: 590.7 E(): 5.4e-25  
96.6% identity in 89 bp overlap

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280      290      300      310      320      330
Sa301248_000 TTCCTGAGGGTAAATATCCTCCTGGNCGACGCGGCCGCTCGAGTCTAGAGGGCCCGTTTA
X02662      TCATCATCATTGAGTTTATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTA
                2620      2630      2640      2650      2660      2670

340      350      360      370      380      390
Sa301248_000 AACCCGCTGATCAGCCTCGACTGTGCCTTCTANTTGCCANCCATNTGTTGTTTGCCCCCT
X02662      AACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTC
                2680      2690      2700      2710      2720      2730

X02662      CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCCTGTCCTTTCTAATAAAATGA
                2740      2750      2760      2770      2780      2790
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Same as AF 060226  
SA 181782

